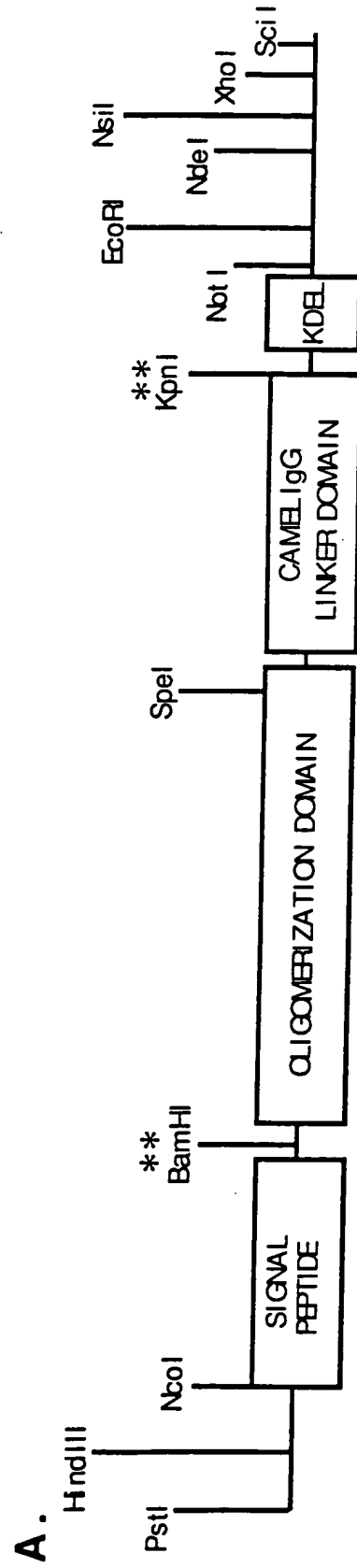


Figure 1: Schematic Representation of KDEL Receptor-Inhibitor Protein and Its Amino Acid Sequences
(Rat COMP oligomerization domain)



B.

Signal cleavage site

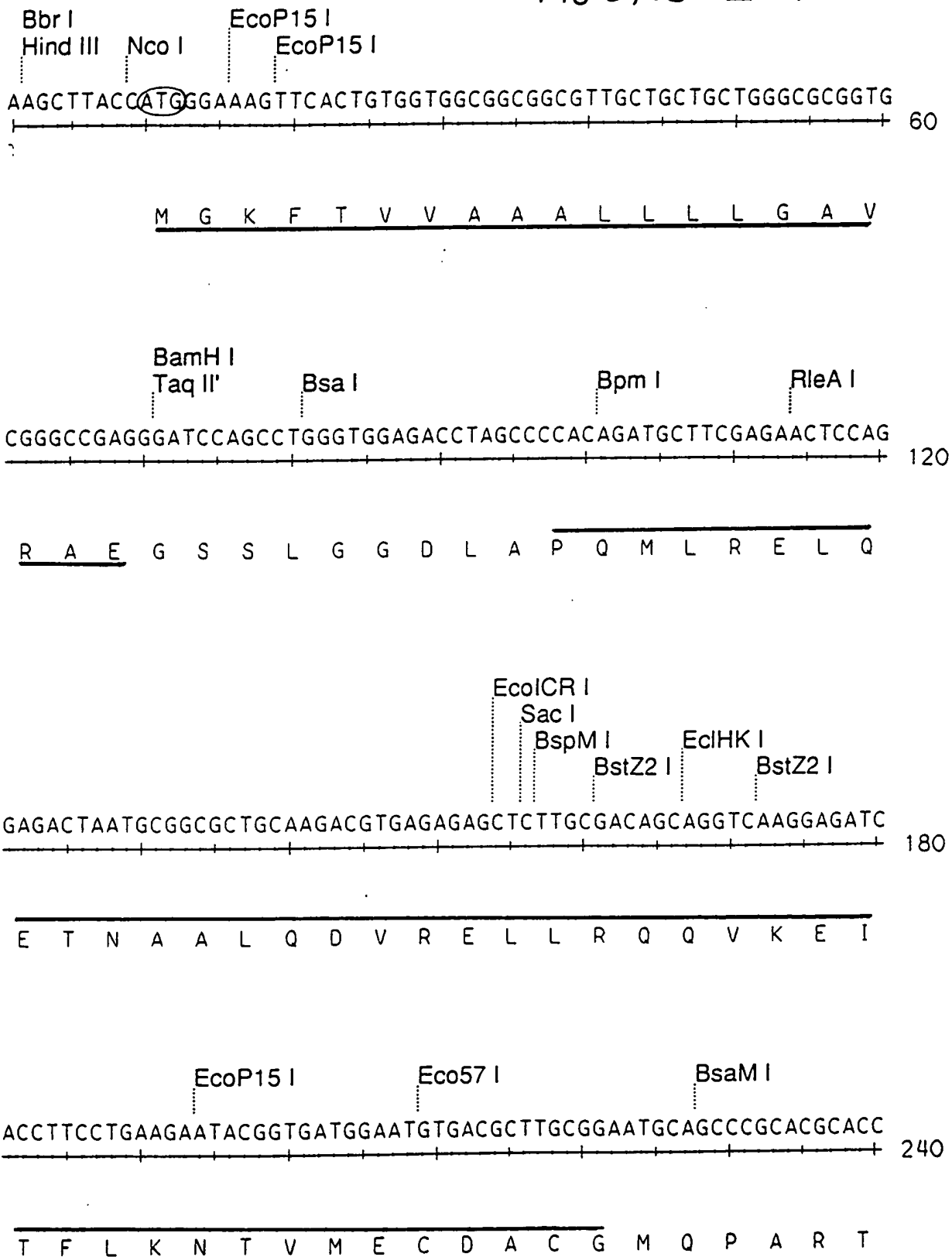
MGKFTVVAALLLLGAVRAE-GSS -

LGGDLA-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

3148 (sheet 2 of 5)

FIGURE 1C.



3. f8 (sheet 3 of 2)

Spe I

CCCGGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAA 300

P G T S P Q P Q P K P Q P Q P Q P Q P K

Acc65 I

Kpn I

Eco52 I

CCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAGGCG 360

P Q P K P E P E G T G S S E K D E L

FIGURE 1D.

Nde I

Ppu10 I

BfrB I

Nsi I

Xho I

Sci I

EcoR I

GCCGCAGAATTCCATATGCATCTCGAG 387

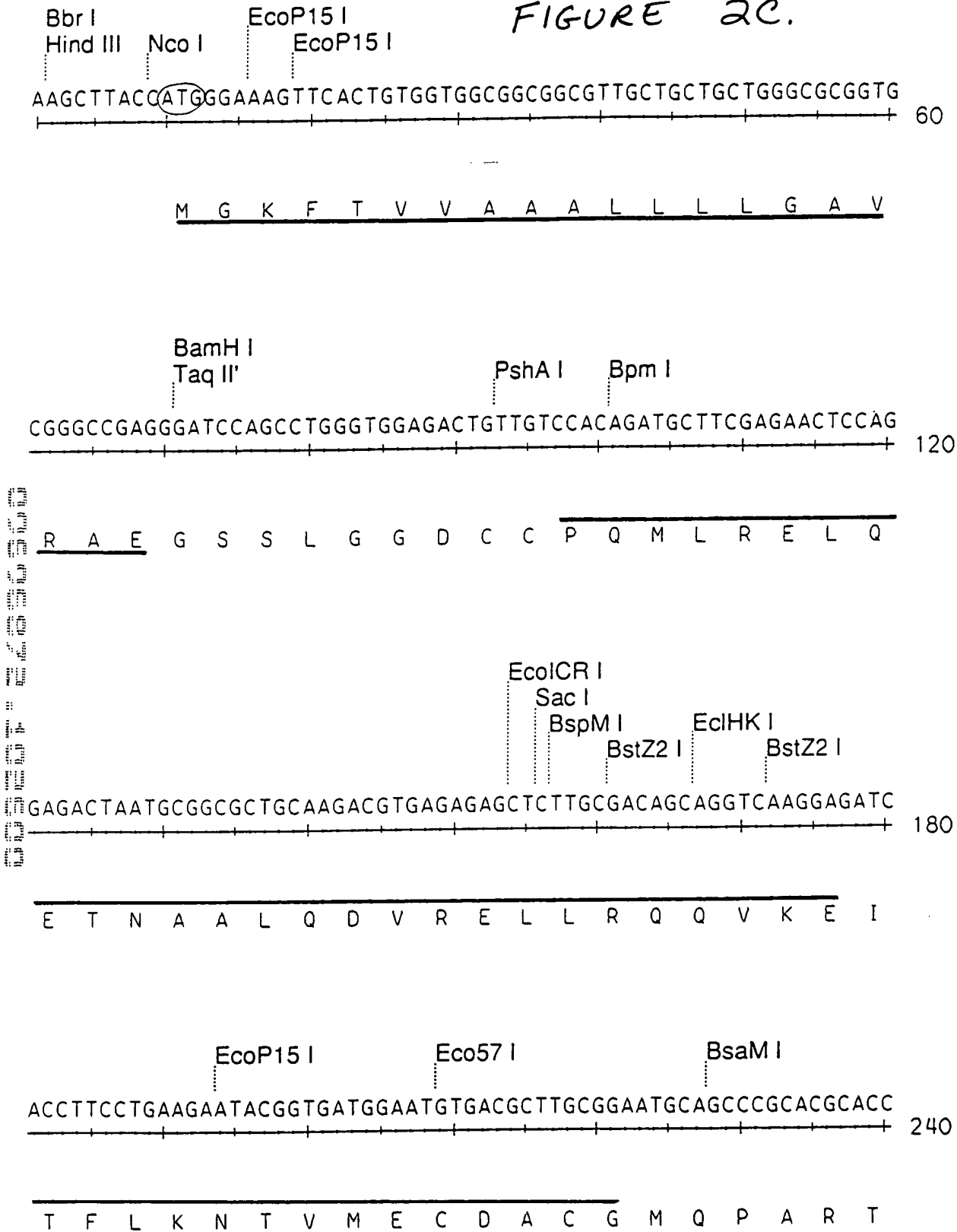
[illegible]

Signal cleavage site

POQPKPQPPQPKPQPKPEPE-GTGSSE-KDEL

31 '88 (sheet 5 of 30)

FIGURE 2C.



318 (sheet 6 of 30)

Spe I

CCCGGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAA 300

P G T S P Q P Q P K P Q P Q P Q P K

Acc65 I

Kpn I

Eco52 I

CCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAGGCG 360

P Q P K P E P E G T G S S E K D E L .

FIGURE 2D.

Nde I

Ppu10 I

BfrB I

Nsi I

Xho I

Sci I

EcoR I

GCCGCAGAATTCCATATGCATCTCGAG 387

[illegible]

3. 188 (sheet 7 of 30)



MGKFTVVA AALLLGAVRAE-GSS-

LGGDCC-KALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPKPQPQPQPQPKPPE-GTGSSE-KDEL

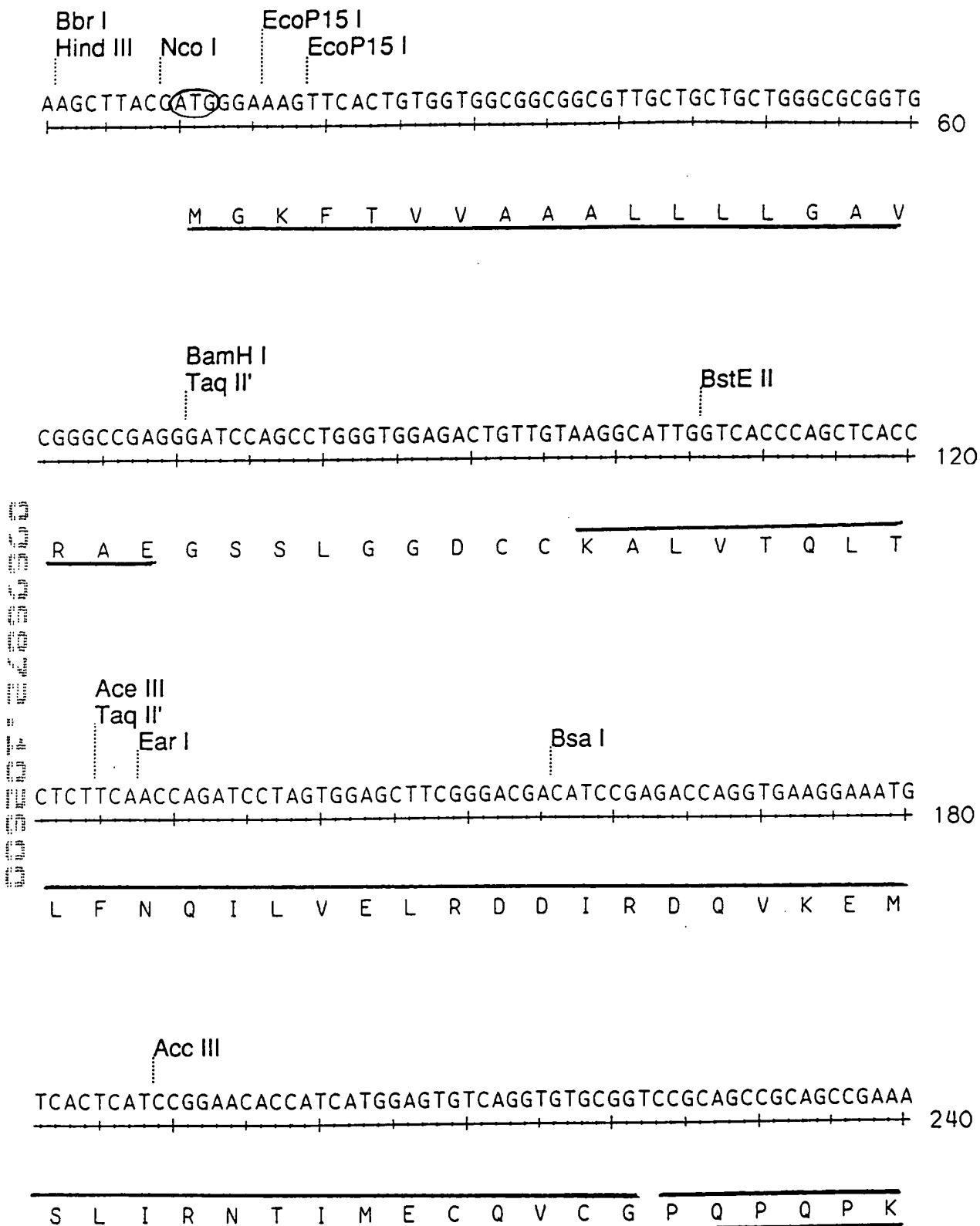


FIGURE 3C.

3148 (sheet 9 of 30)

CCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACC 300
Acc65 I
Kpn I

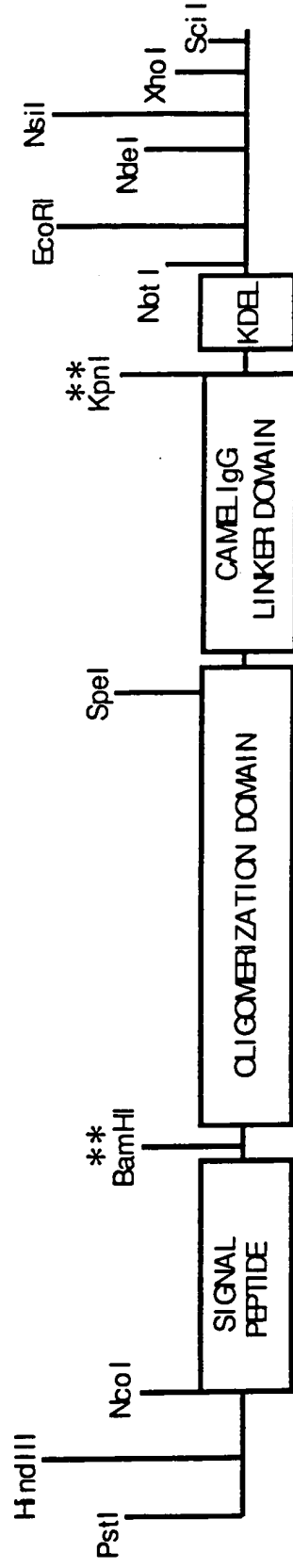
P Q P Q P Q P Q P K P Q P K P E P E G T

GGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATGCATCTCGAG 357
Eco52 I EcoR I Nde I Ppu10 I BfrB I Nsi I Xho I Sci I
G S S E K D E L

FIGURE 3D

Figure 4: MOUSE TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site



MGKFTVAAALLLGA VRAE-GSS -

LGGDCC-GEQTKAL VTQLTLFNQIL VELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQKPQPQPQPQPQKPEPE-GTGSSE-KDEL

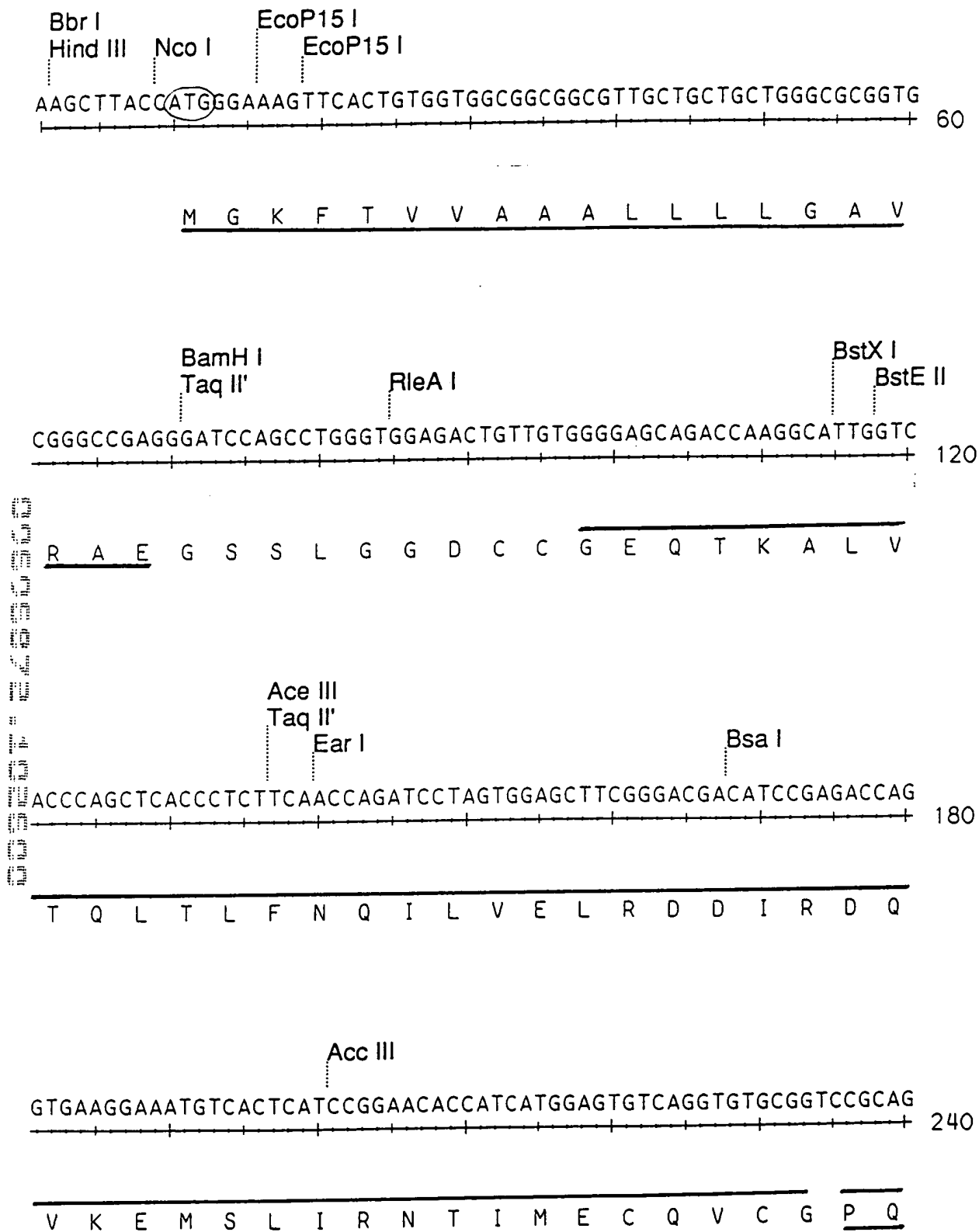


FIGURE 4C.

31.88 (sheet 12 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG TAG GCGGCCGCAGAATTCCATATG 360

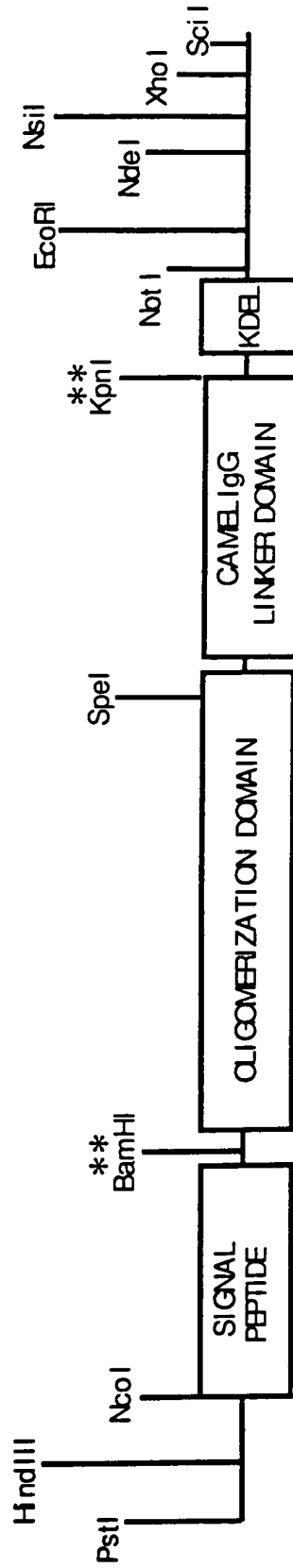
P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 4D.

Figure 5: XENOPUS TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site

MGKFTVVAALLLGAVRAE-GSS -

LGGDCC-GDVSRQLIGQITQMNQMLGELRDVMRQQVKETMFLRNTIAECQACG-

PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

488 (sheet 1 of 30)

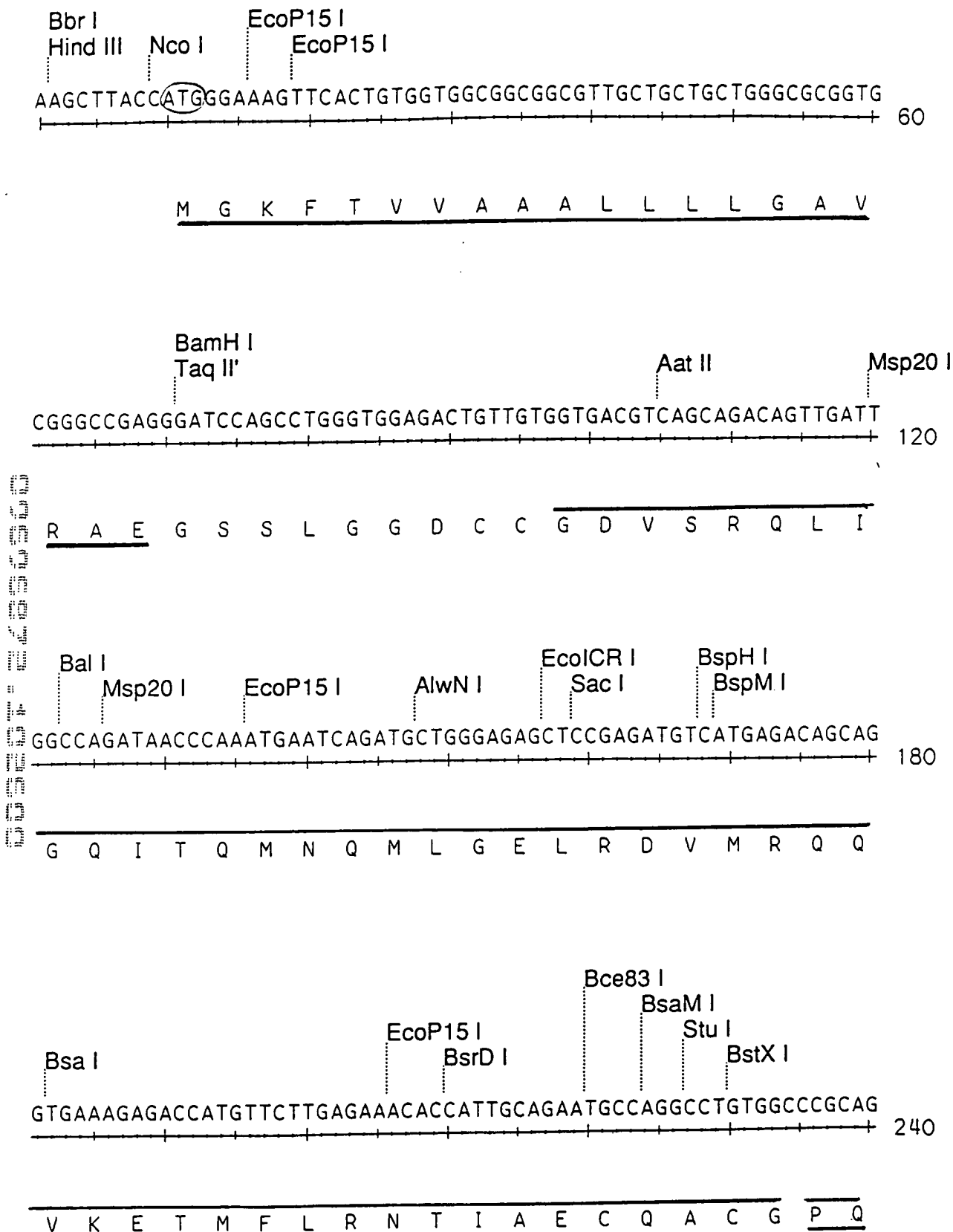


FIGURE 5C

31408 (sheet 15 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

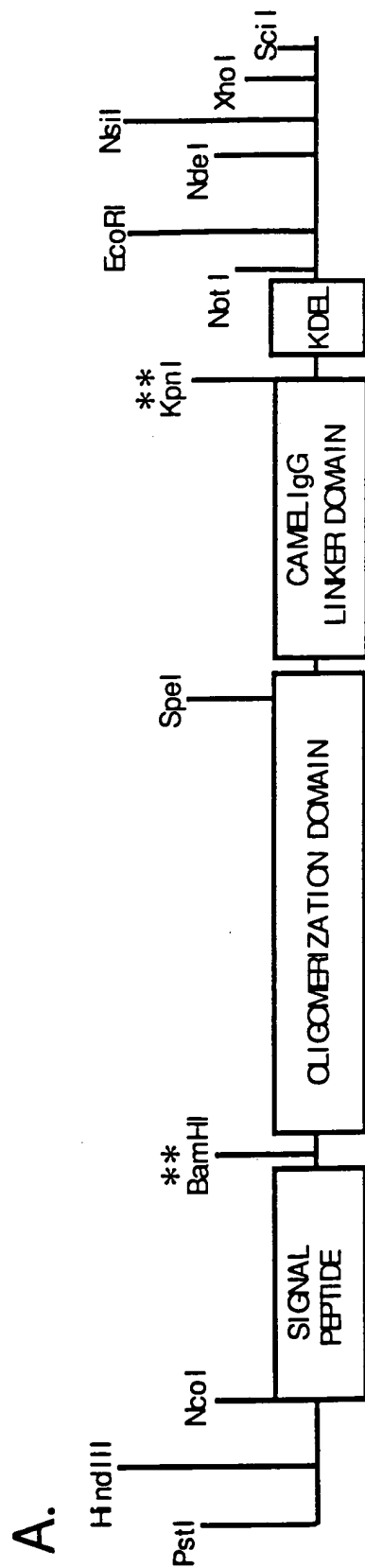
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360
ATAC

P E G T G S S E K D E L .

FIGURE 5D.

Nsi I Xho I Sci I
CATCTCGAG 369

Figure 6: HUMAN COMP OLIGOMERIZATION DOMAIN
KDEL RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

↓

MRYMILGLLALAAVCSAAKK-GSS-

LGGDCC-SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG-

PQPQPKPQPQPQPQPQPQPPEPE-GTGSSE-KDEL

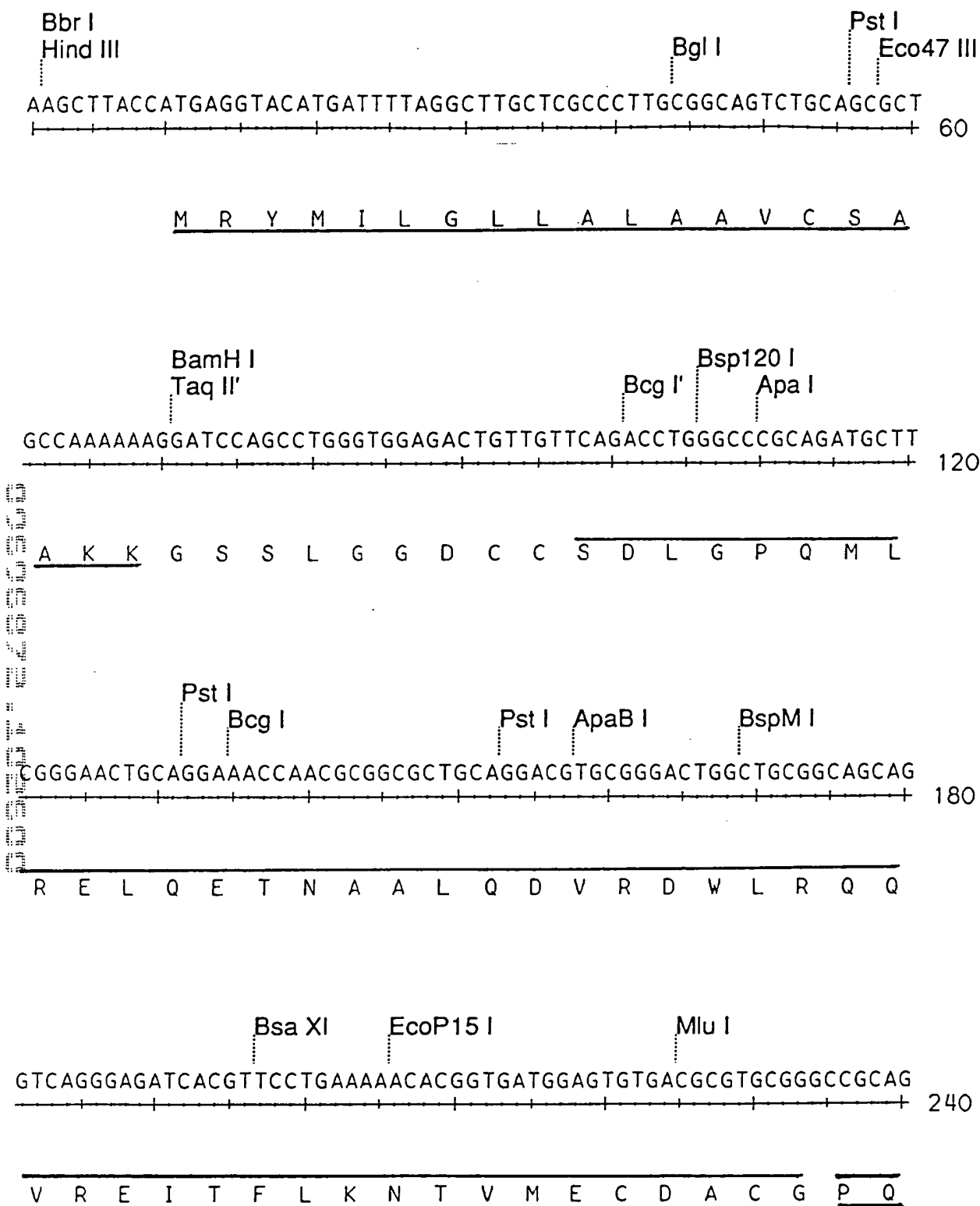


FIGURE 6C.

3188 (sheet 18 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

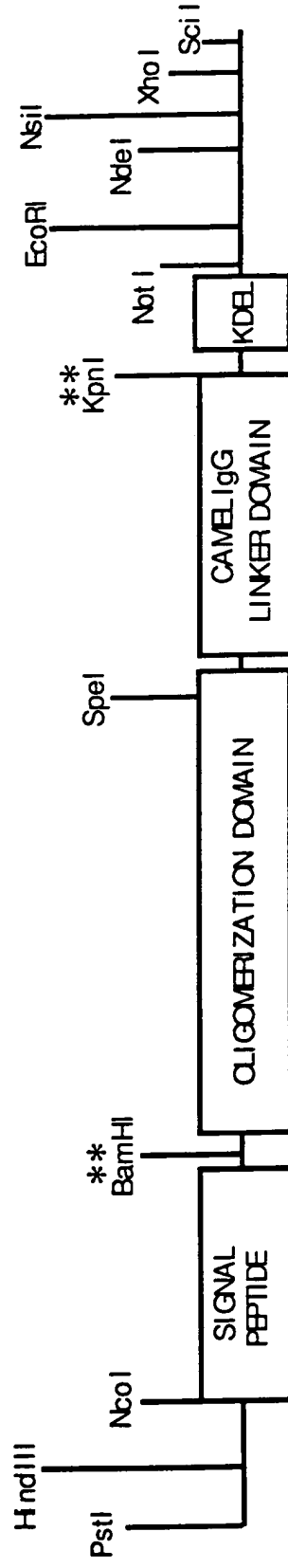
P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 6D.

Figure 7: HUMAN PLB OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN

A.



B.

Signal cleavage site
 MRYMILGLLAAVC**SA**AKK-GSS -
 LGDCC-QKLQNLFINFLICLLICLIIVMLL-
 PQPKPQPKPQPKPQPKPEPE-GTGSSE-KDEL

- Residues critical for pentamer formation

388 (sheet 2 of 30)

Bbr I
Hind III

Bgl I

Pst I
Eco47 III

AAGCTTACCATGAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCT 60

M R Y M I L G L L A L A A V C S A

BamH I
Taq II'

PshA I

GCCAAAAAAGGATCCAGCCTGGGTGGAGACTGTTGTCAAAAGCTACAGAATCTATTTATC 120

A K K G S S L G G D C C Q K L Q N L F I

BsaB I

AATTTCTGTCTCATCTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCTCCCG 180

N F C L I L I C L L L I C I I V M L L P

CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG 240

Q P Q P K P Q P Q P Q P Q P K P Q P K P

FIGURE 7C.

1488 (sheet 2 of 30)

Acc65 I Kpn I Eco52 I EcoR I Nde I

GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT 300

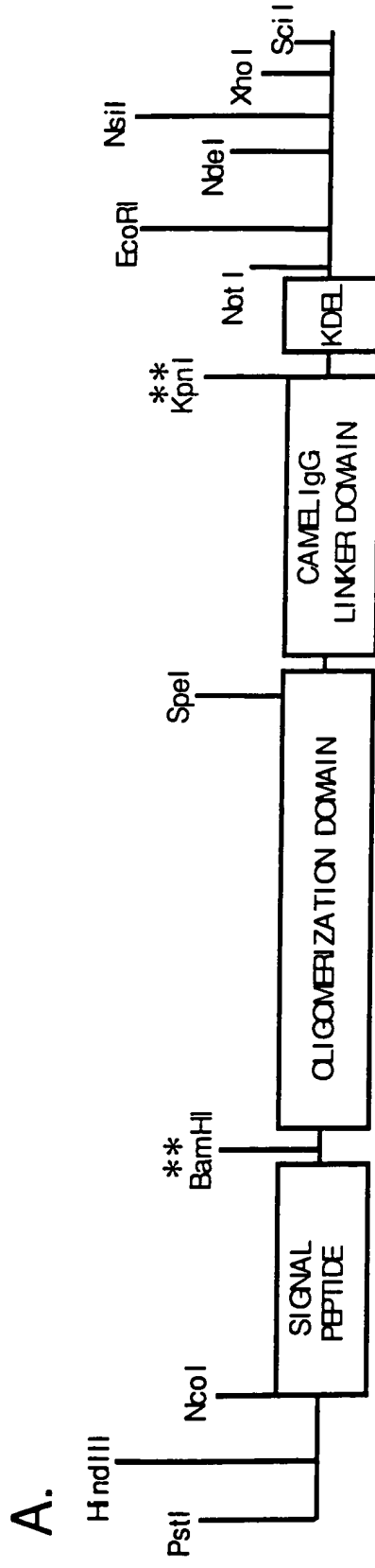
E P E G T G S S E K D E L .

Ppu10 I
BfrB I
Nsi I
Xho I
Sci I

ATGCATCTCGAG 312

FIGURE 7D.

Figure 8: HUMAN TSP3 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

MRYMILGLLALAAVCSAAKK-GSS -
LGGDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-
PQPQKPQPQPQPQPKPQKPEPE-GTGSSE-KDEL

1488 (sheet 2 of 30)

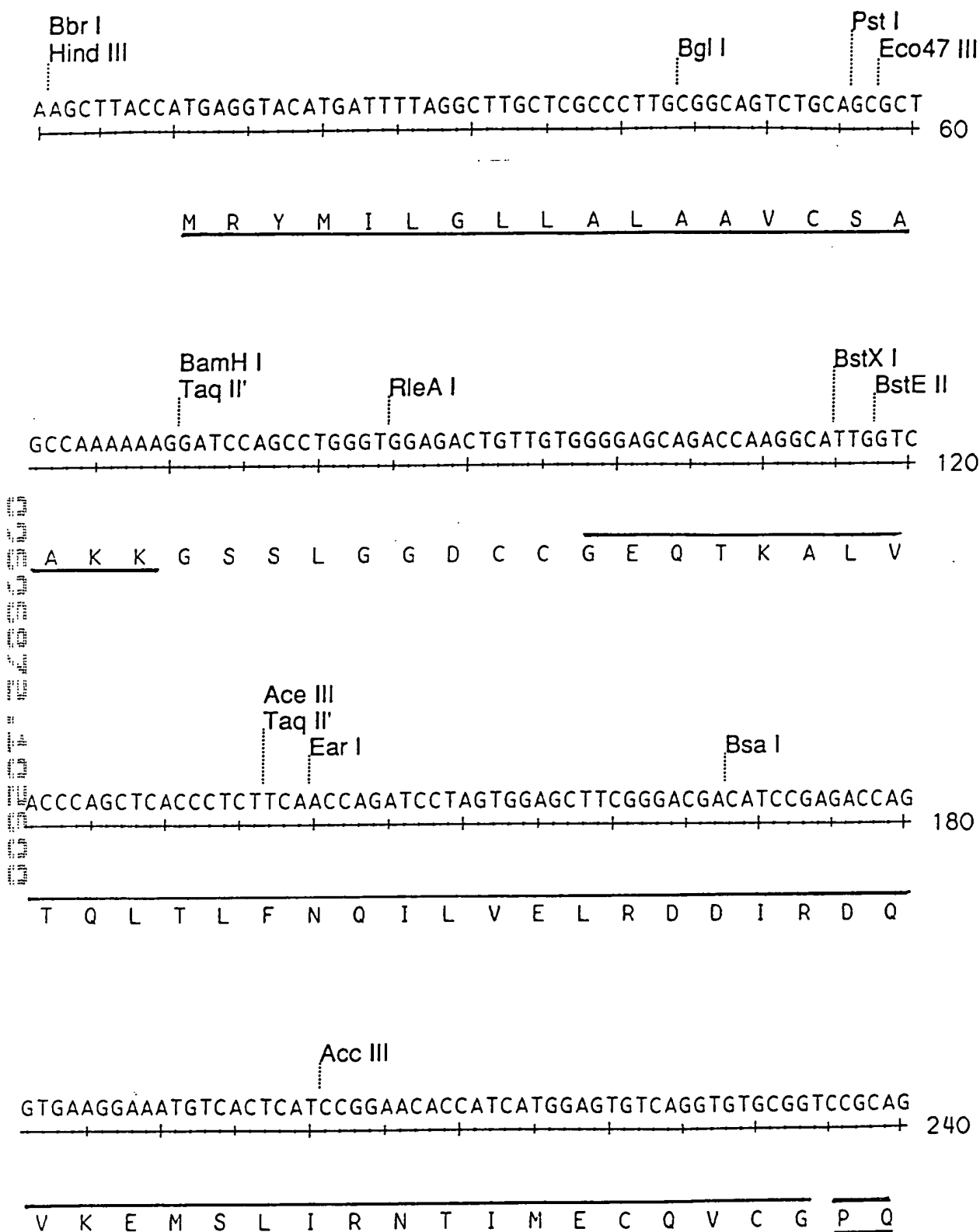


FIGURE 8C.

3148 (sheet 24 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

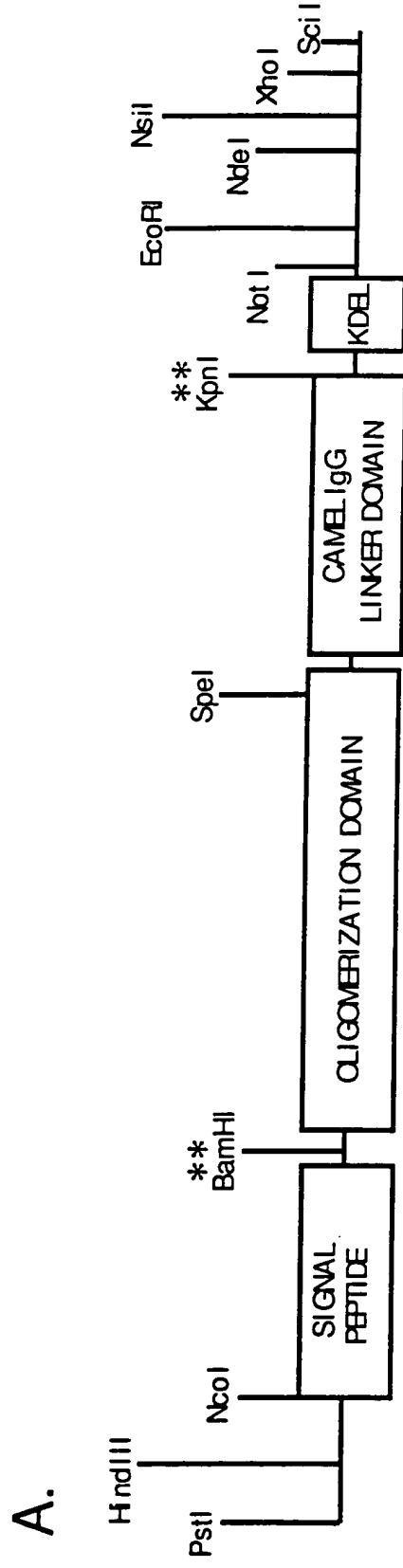
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 8D.

Figure 9: HUMAN TSP4 OLIGOMERIZATION DOMAIN KDEL
RECEPTOR INHIBITOR PROTEIN



B.

Signal cleavage site

↓

MRYMILGLLALAAVCSAAKK-GSS -

LGGDCC-GDFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFRLRNTIAECQACG-

PQPQPKPQPQPQPQPKPQPKPEPE-GTGSSE-KDEL

1488 (sheet 2 of 30)

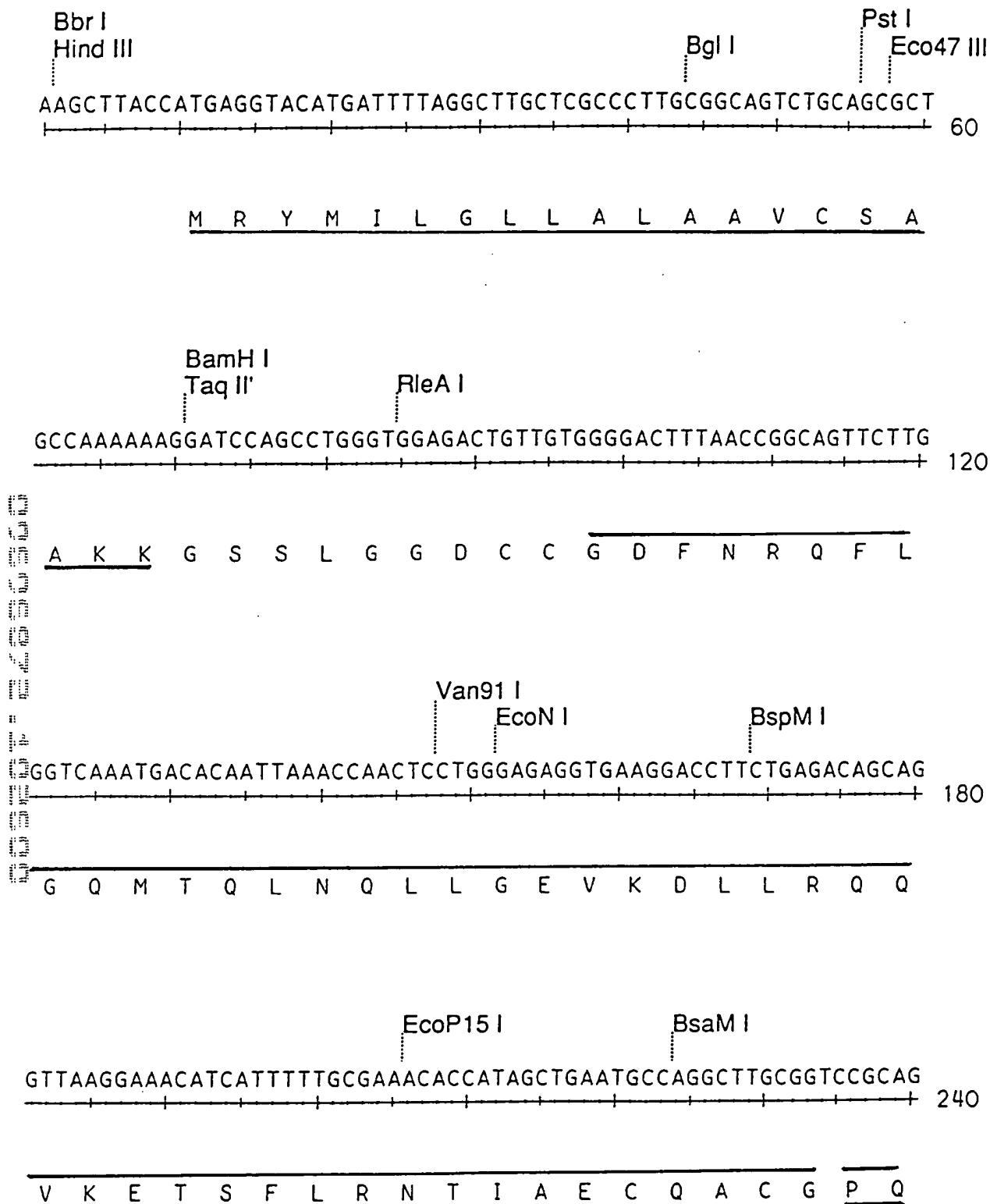


FIGURE 9C.

3488 (sheet 27 of 30)

CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P K P Q P K P E

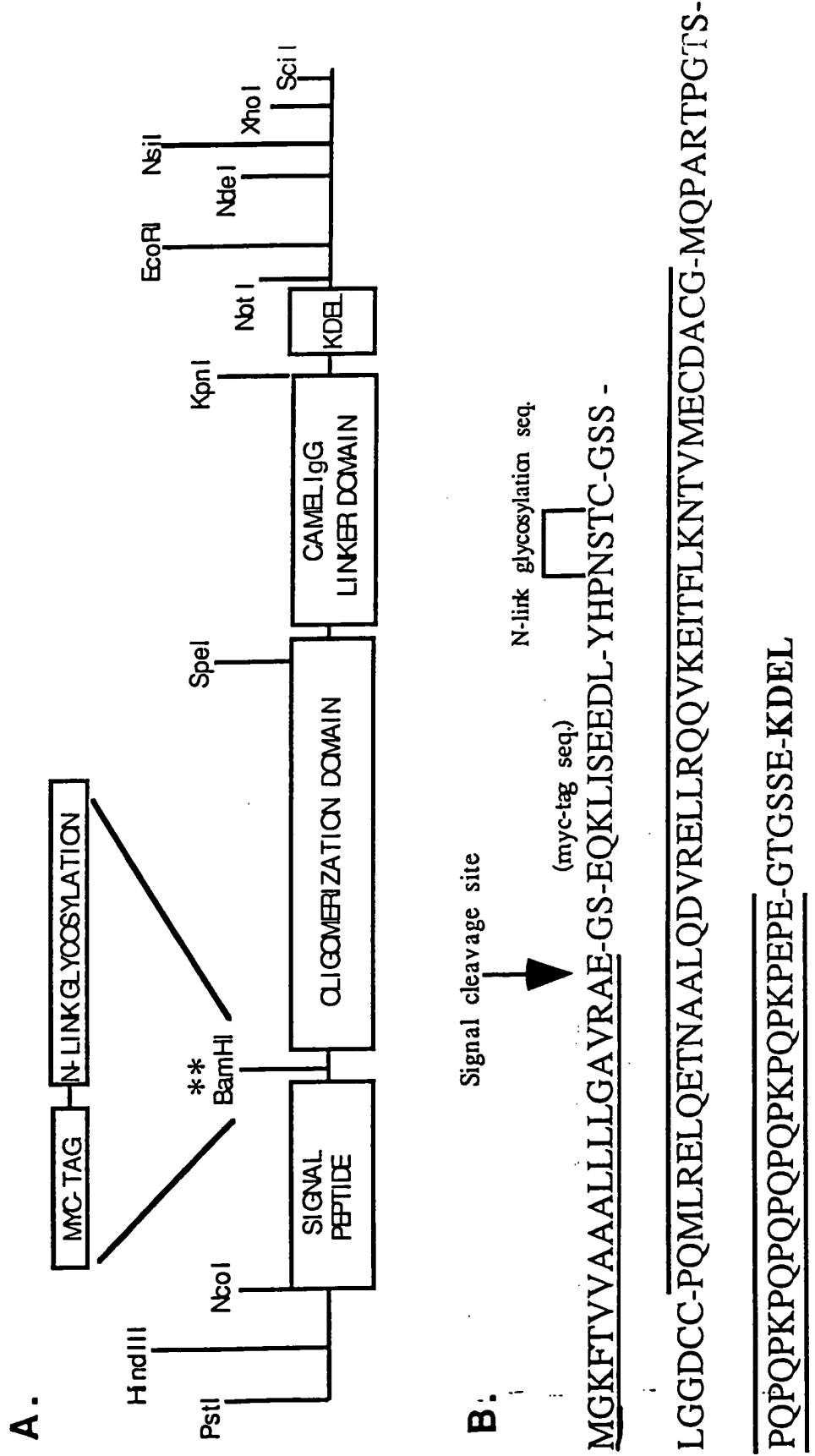
Acc65 I Kpn I Eco52 I EcoR I Nde I Ppu10 I BfrB I
CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATG 360

P E G T G S S E K D E L .

Nsi I Xho I Sci I
CATCTCGAG 369

FIGURE 9D.

Figure 10: KDEL Inhibitor Protein with myc-tag and a N-linked Glycosylation Sequence



34 is (sheet 29 ~ 30)

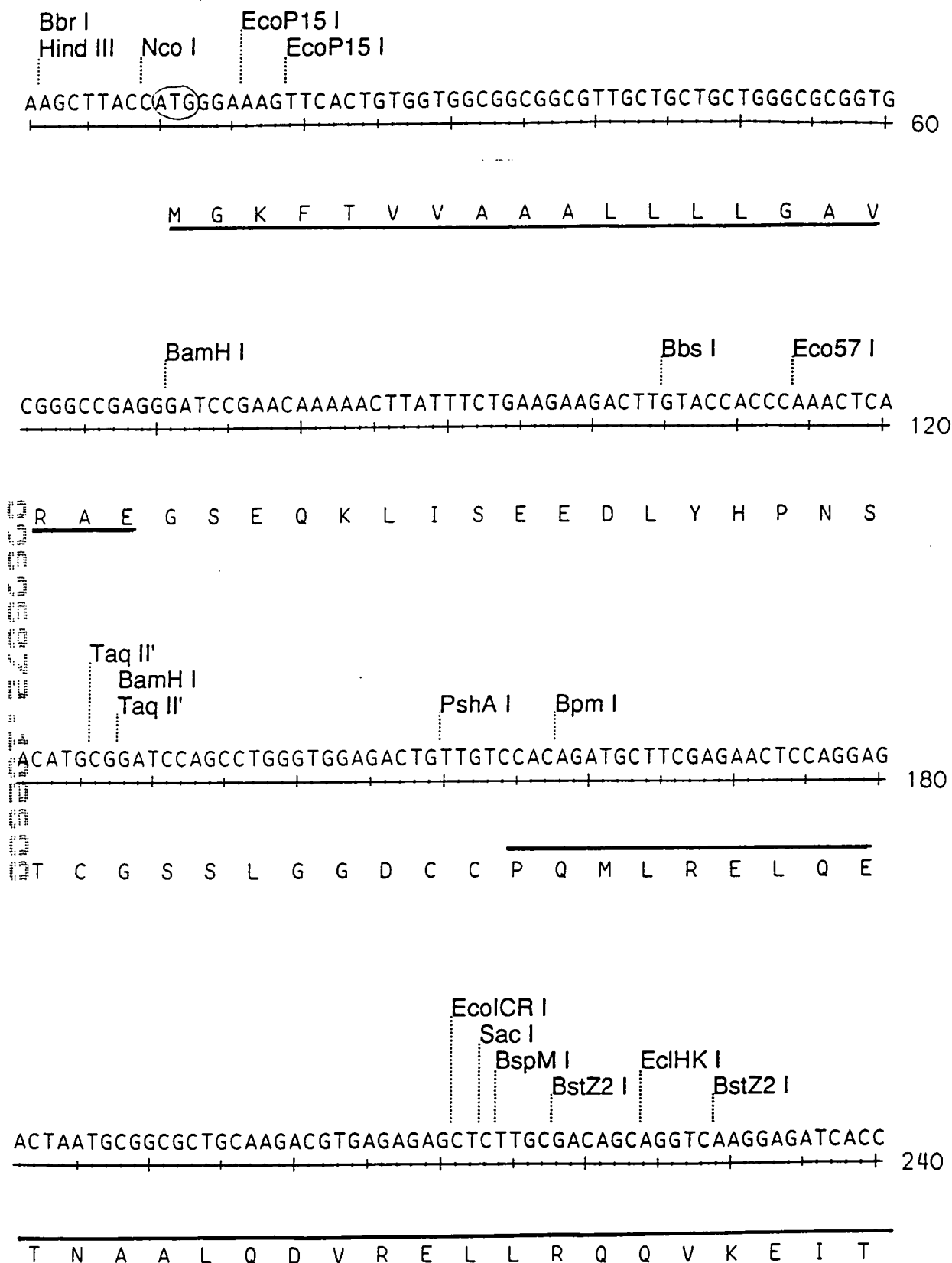


FIGURE 10C.

3188 (sheet 30 of 30)

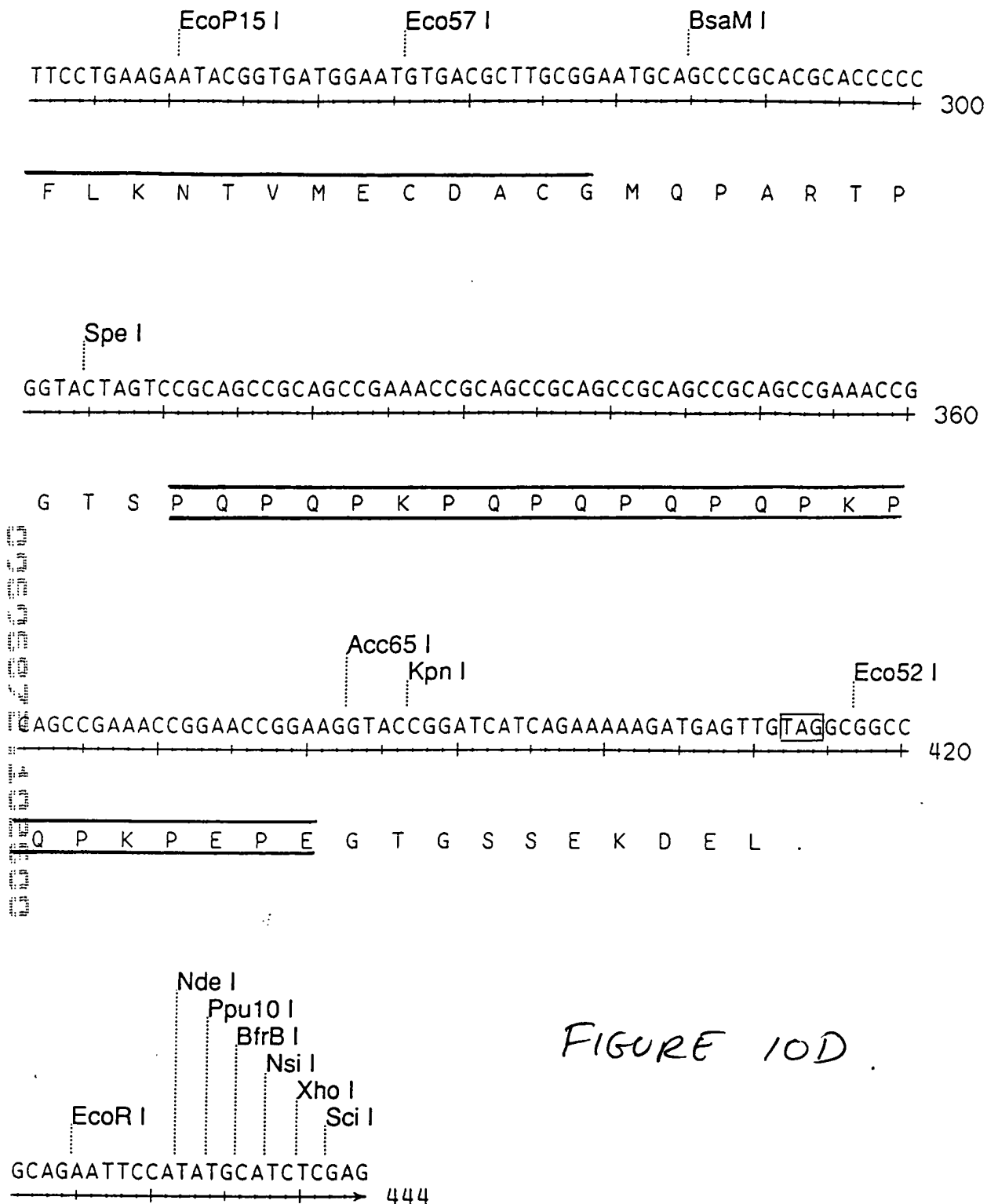


FIGURE 10D .

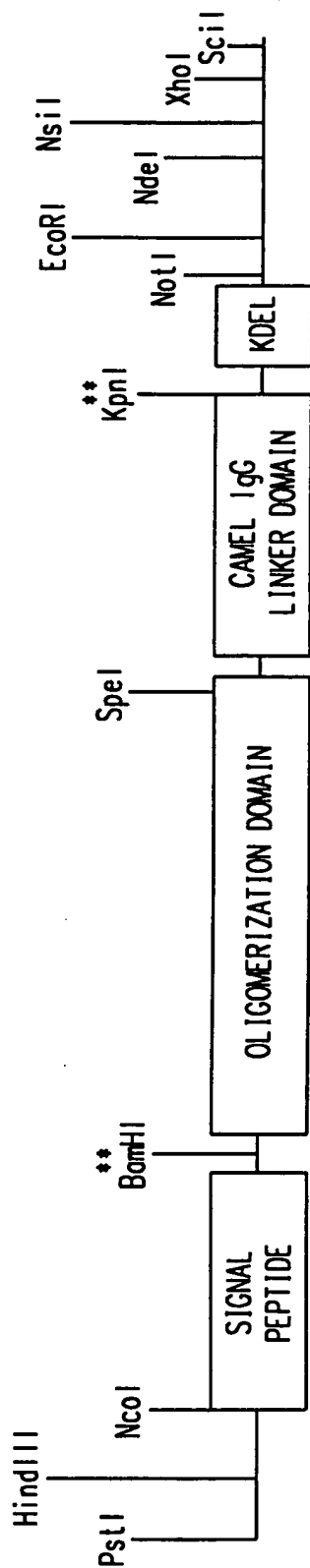


FIG. 1A

SIGNAL CLEAVAGE SITE

MGKFTVVAALLLGAVRAE-GSS-

LCGDLA-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQPKPQQPPQPKPEPE-GTGSSE-KDEL

FIG. 1B

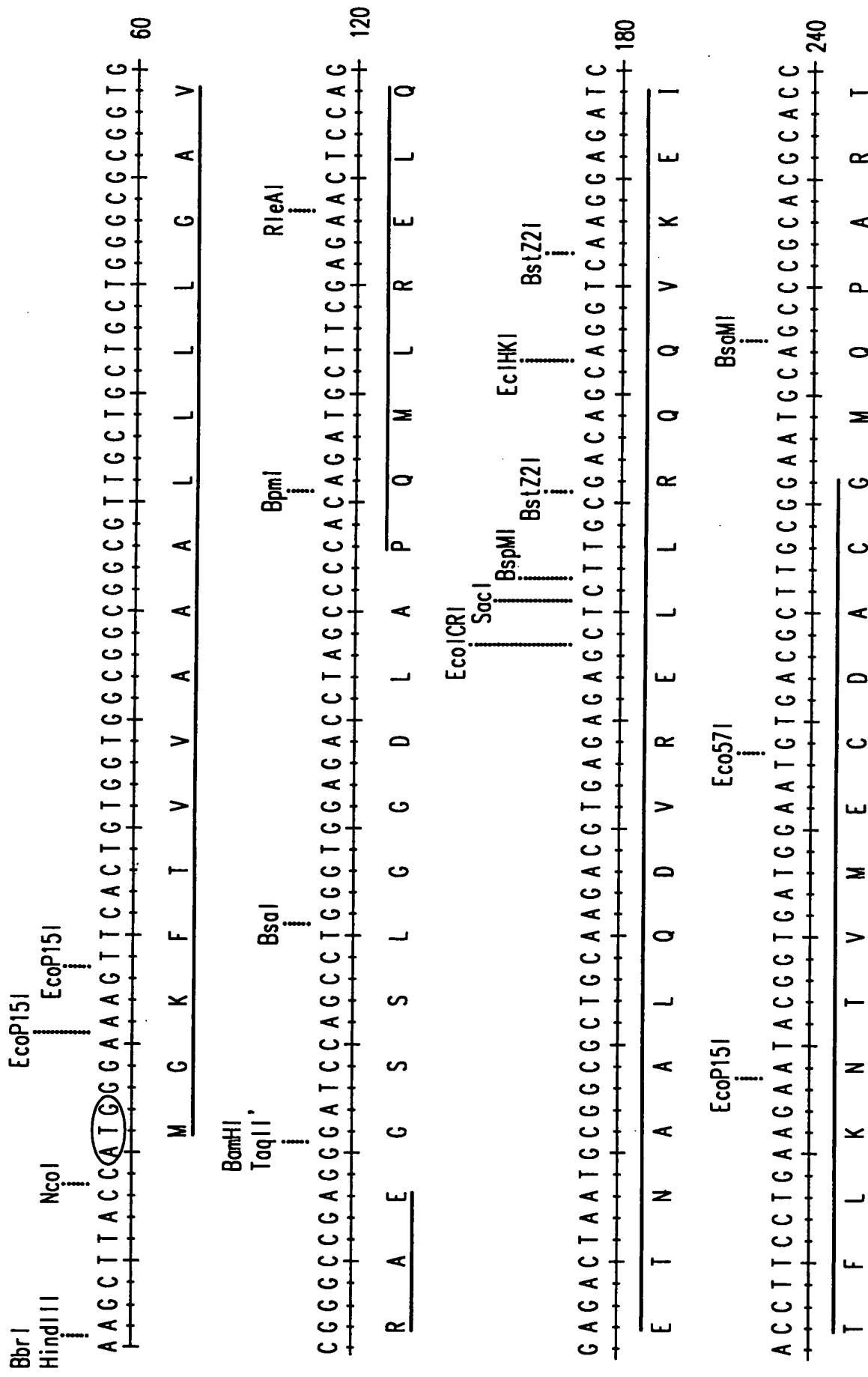


FIG. 1C

SpeI
 C C C G G T A C T A G T C C G C A G C C G C A G C C G A A A C C G C A G C C G C A G C C G C A G C C G A A 300
 P G T S P Q P Q P K P Q P Q P Q P Q P K
 C C G C A G C C G A A A C C G G A A C C G G A T C A C G A T C A G A A A G A T G T G T A G G C C G 360
 Eco52I
 Eco65I KpnI
 P Q P K P E P E G T G S S E K D E L
 NdeI Ppu10I
 BfrBI NsiI XhoI
 EcoRI SclI
 G C C G C A G A A T T C C A T A T G C A T C T C G A G 387

Age Group	Percentage
18-24	~10%
25-34	~10%
35-44	~10%
45-54	~10%
55-64	~10%
65-74	~10%
75-84	~15%
85+	~5%

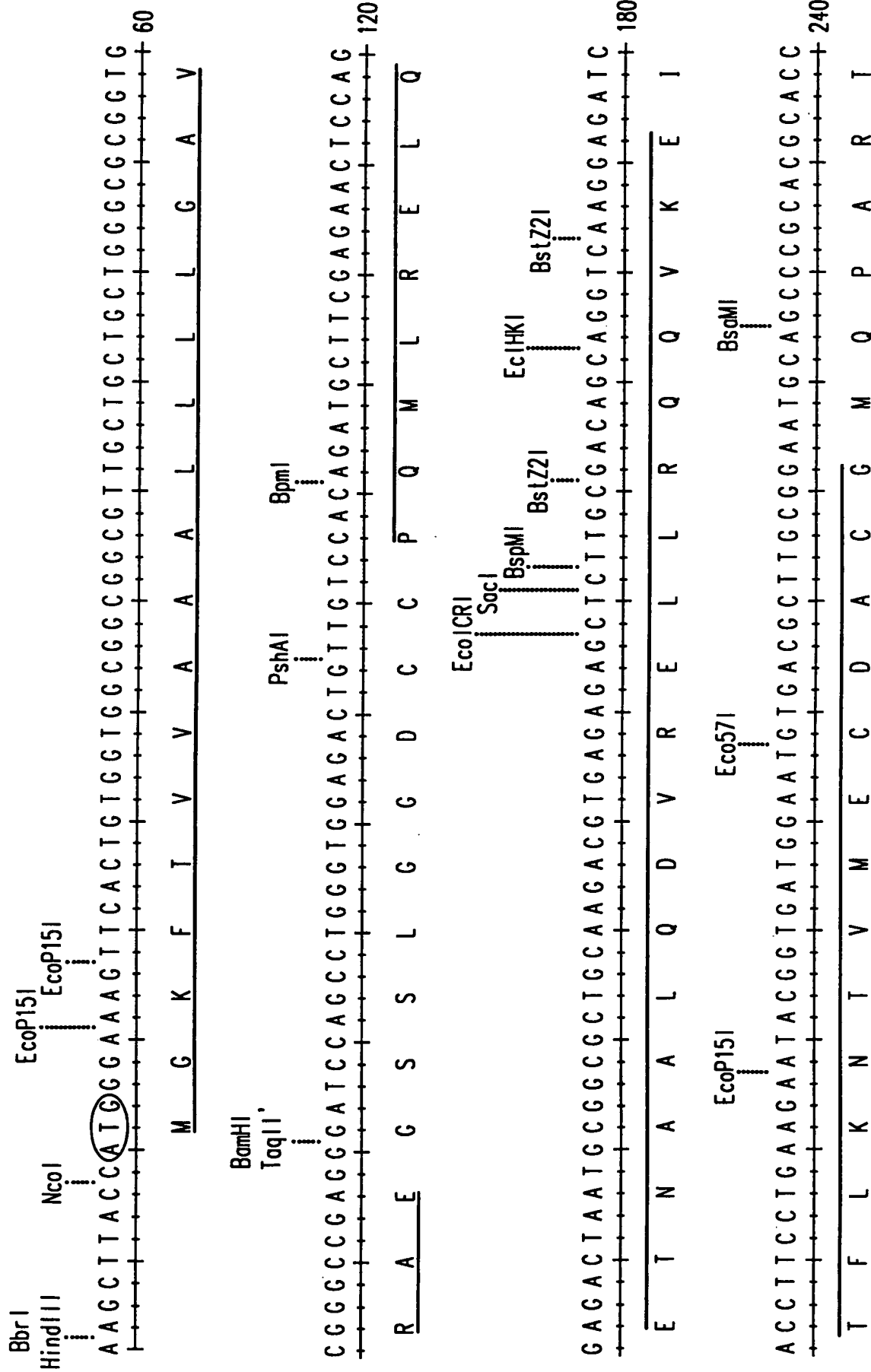
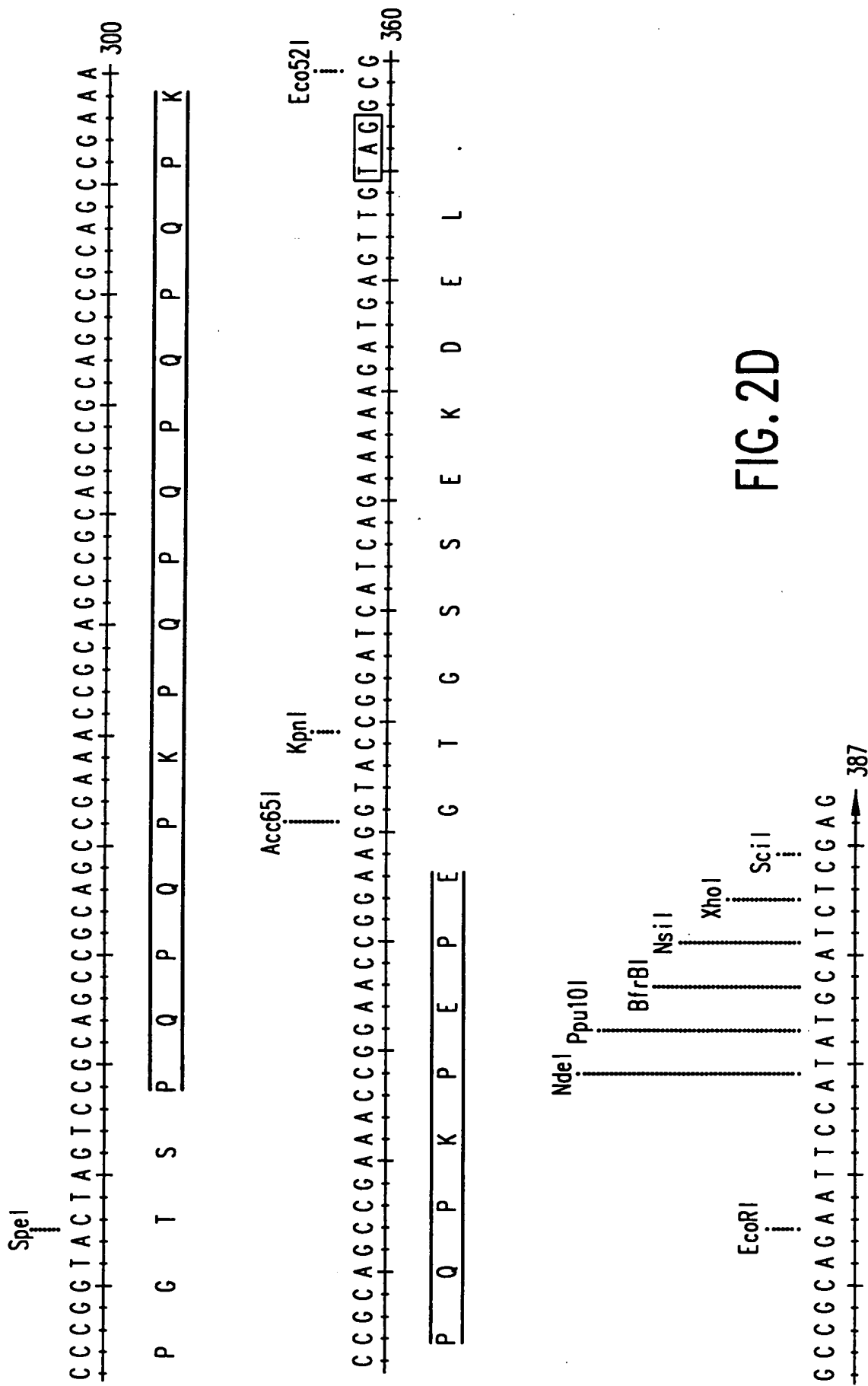


FIG. 2C



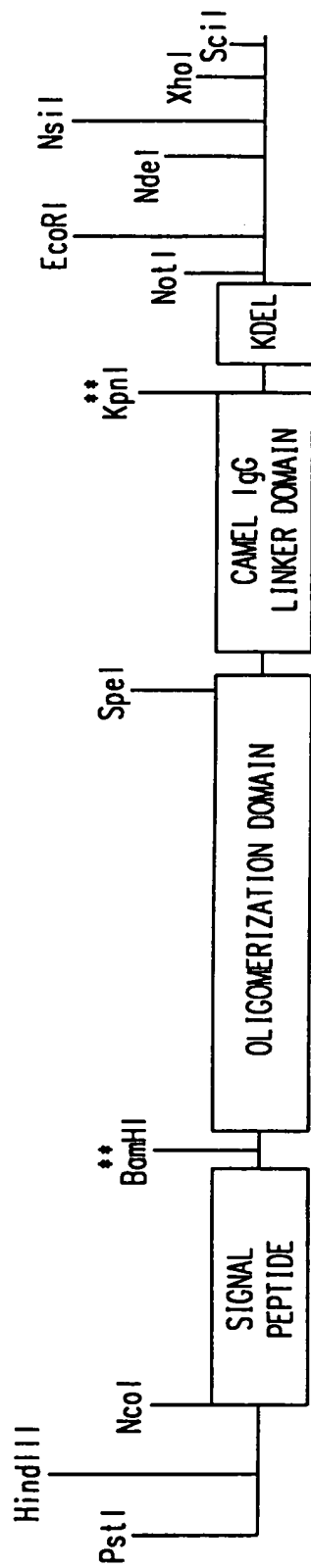


FIG. 3A

SIGNAL CLEAVAGE SITE
 ↓
M G K F T V A A A L L L G A V R A E - G S S -

L G G D C C - K A L V T Q L T L F N Q I L V E L R D D I R D Q V K E M S L I R N T I M E C Q V C G -
P Q P Q K P Q P Q P Q P Q P K P E P E - G T G S S E - K D E L

FIG. 3B

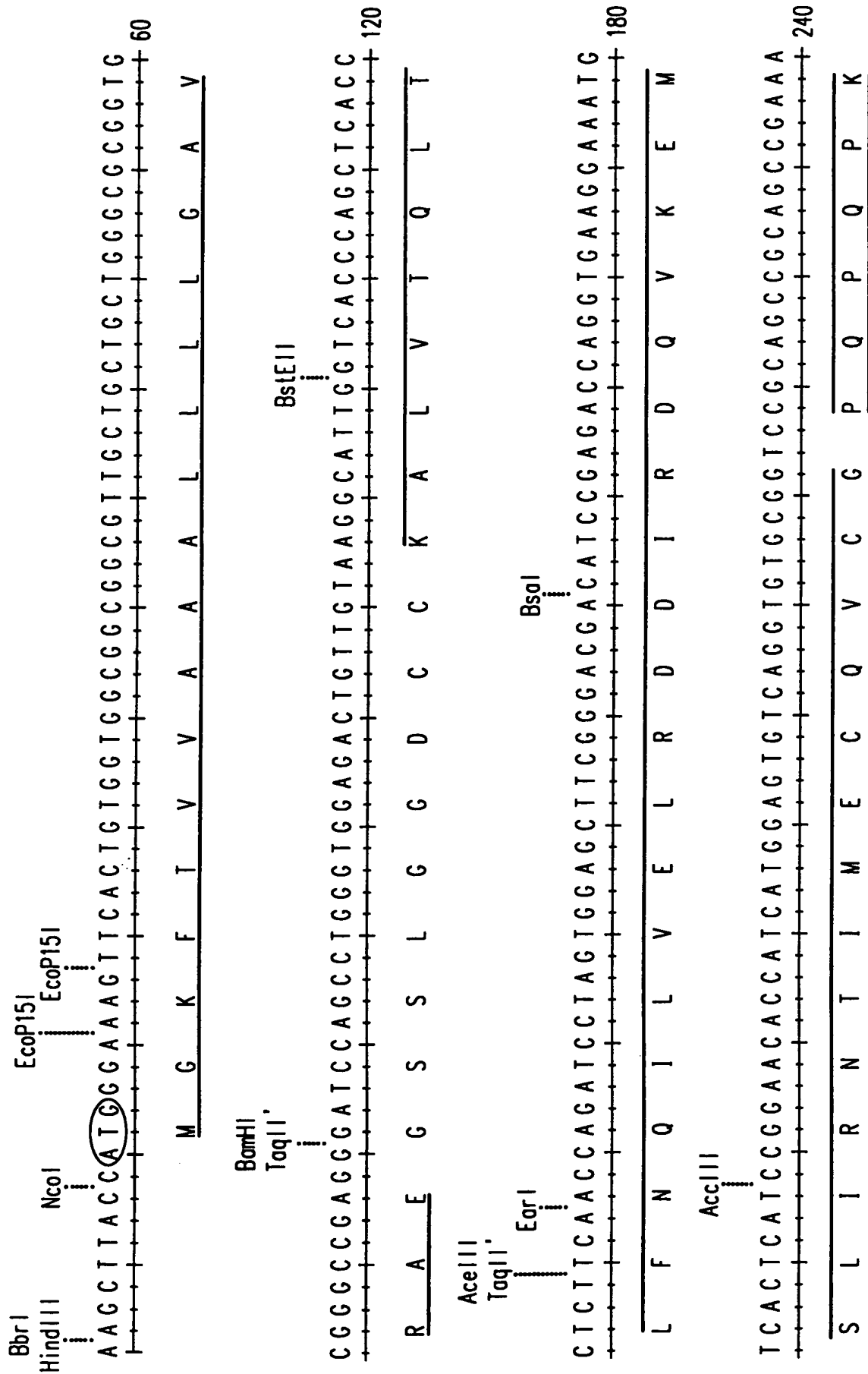


FIG. 3C

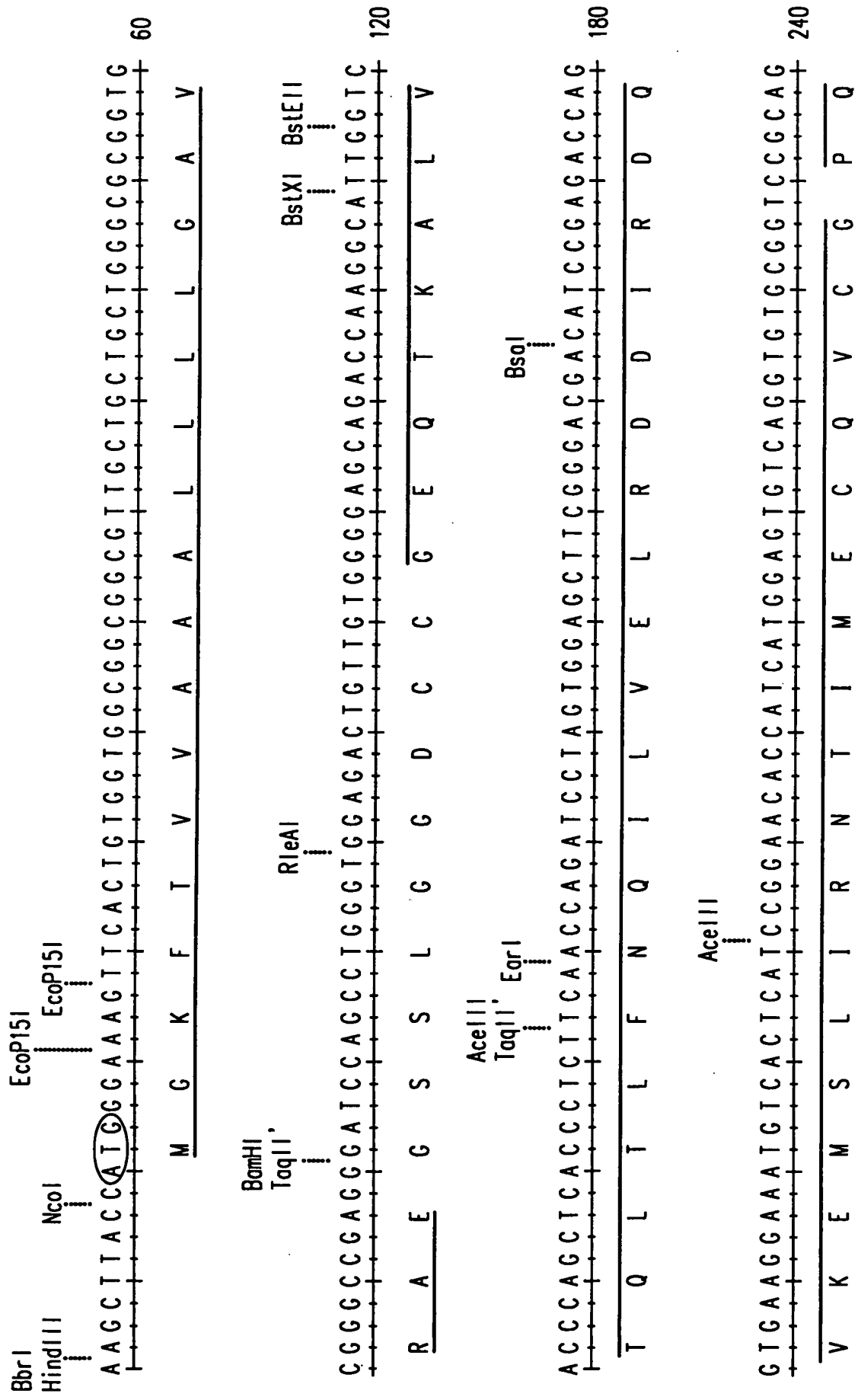


FIG. 4C

CCG CAG CCG GAA ACC CCG CAG CCG CCG CAG CCG CCG CAG CCG CCG GAA ACC CCG CAG CCG CCG GAA ACC CCG GAA

CCG CAG CCG GAA ACC CCG CAG CCG CCG CAG CCG CCG CAG CCG CCG GAA ACC CCG CAG CCG CCG GAA ACC CCG GAA 300

P Q P K P Q P Q P Q P Q P Q P Q P Q P K P E

CCG GAA GGT ACC GGA TCATCAGAAAAGATGAGTTG TAG CCG CCG CCG CAG AATTC CATATG 360

Acc65I KpnI NdeI Ppu10I BfrBI

Eco52I EcoRI

P E G T G S S E K D E L

NsiI XhoI SclI CATCTCGAG 369

FIG. 4D

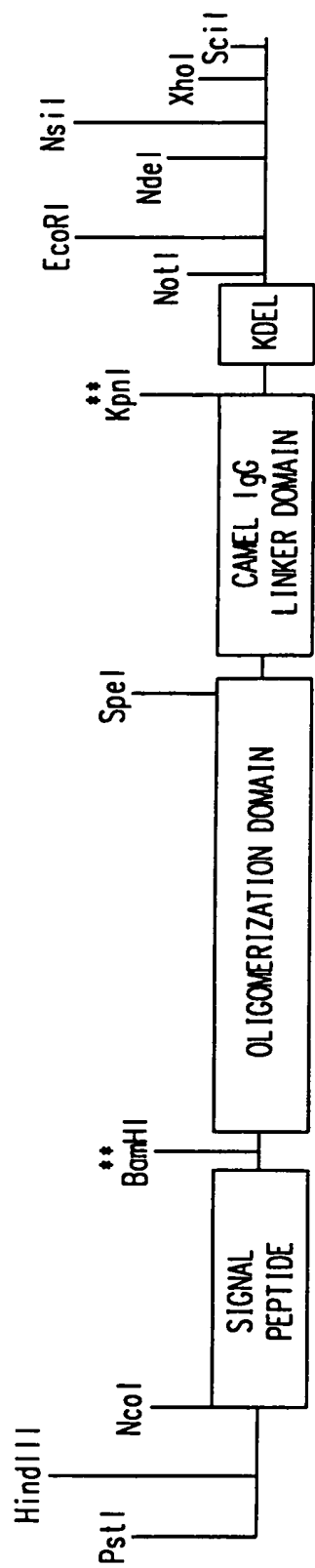


FIG. 5A

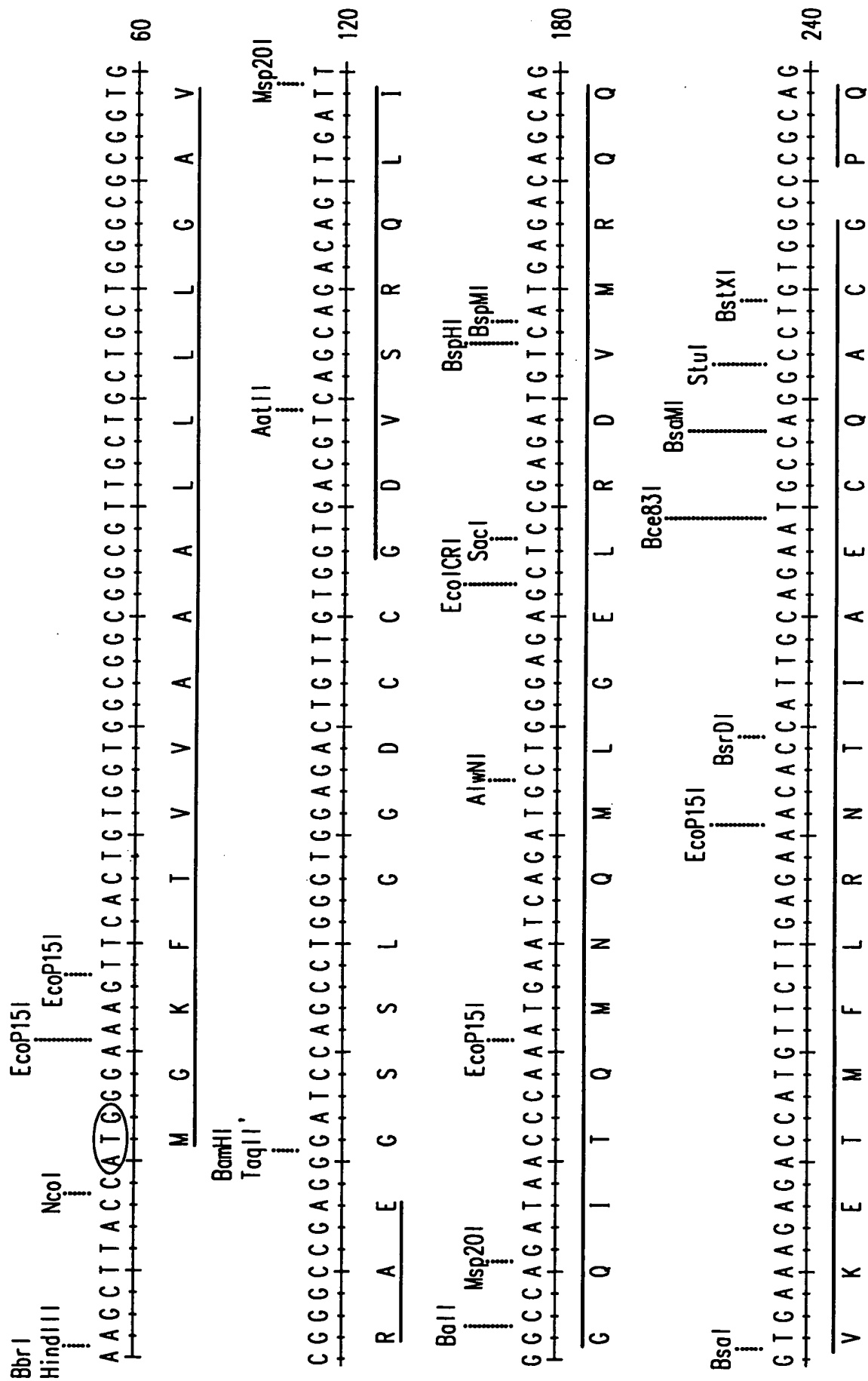
SIGNAL CLEAVAGE SITE

M G K F T V A A A L L L L G A V R A E - G S S -

L G G D C C - G D V S R Q L I G Q I T Q M N Q M L G E L R D V M R Q Q V K E T M F L R N T I A E C Q A C C -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 5B



CCG CAG CCG A A C C G C A G C C G C A G C C G C A G C C G C A A C C G C A G C C G A A C C G G A A 300

P Q P K P Q P Q P Q P Q P Q P Q P K P Q P K P E

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTG[TAG]CCGGCCGCAGCAATTC CATATG 360

NdeI
Ppu10I
BfrBI

Eco52I
EcoRI

ATAC

P E G T G S S E K D E L .

NsiI
XhoI
SciI
CATCTCGAG 369

FIG. 5D

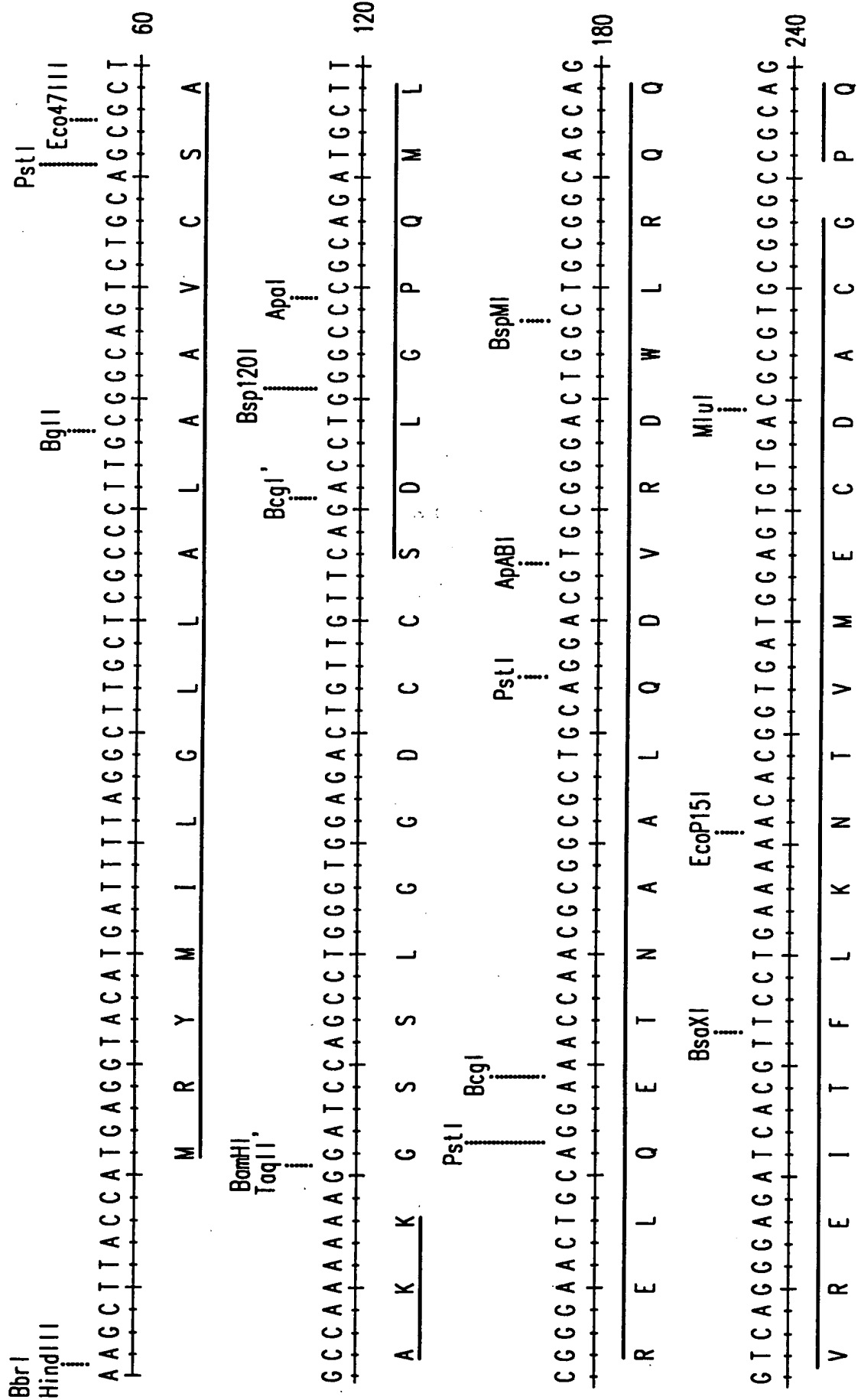


FIG. 6C

P Q P K P Q P Q P Q P Q P Q P Q P Q P Q

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTGTAGCGCGCCGACAAATTCATATG
 NdeI Ppu10I BfrBI
 Eco52I EcoRI
 KpnI Acc65I
 360

P E T R O S E K D E L

Diagram illustrating the DNA sequence CATCTCGAG with restriction sites NsiI, XhoI, and SclI. The sequence is shown with positions 1, 4, 7, and 369 marked. NsiI is at position 1, XhoI at position 4, and SclI at position 7.

FIG. 6D

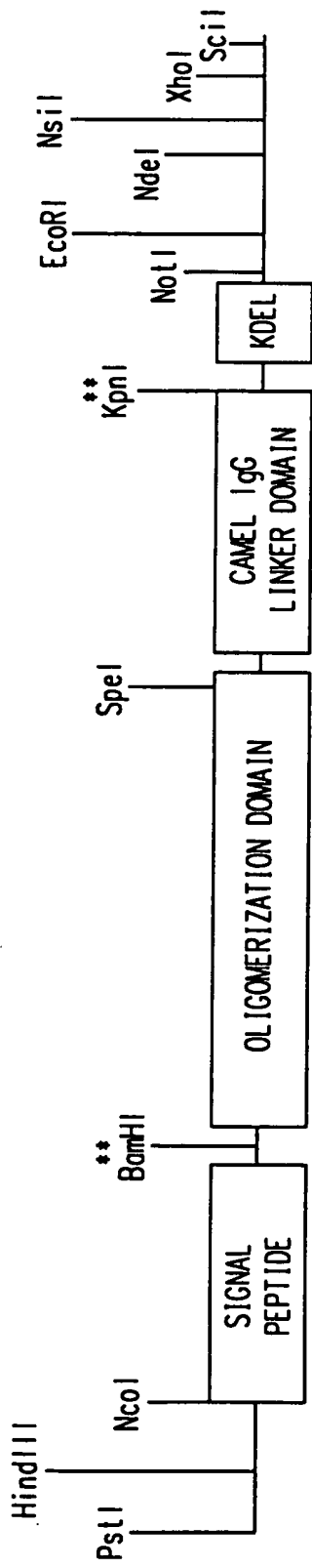


FIG. 7A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - Q K L Q N L F I N F C I L I C L L I C I I V M L L -

P Q P Q K P Q P Q P Q P Q P Q P Q P K P E P E - G T G S S E - K D E L

• RESIDUES CRITICAL FOR PENTAMER FORMATION

FIG. 7B

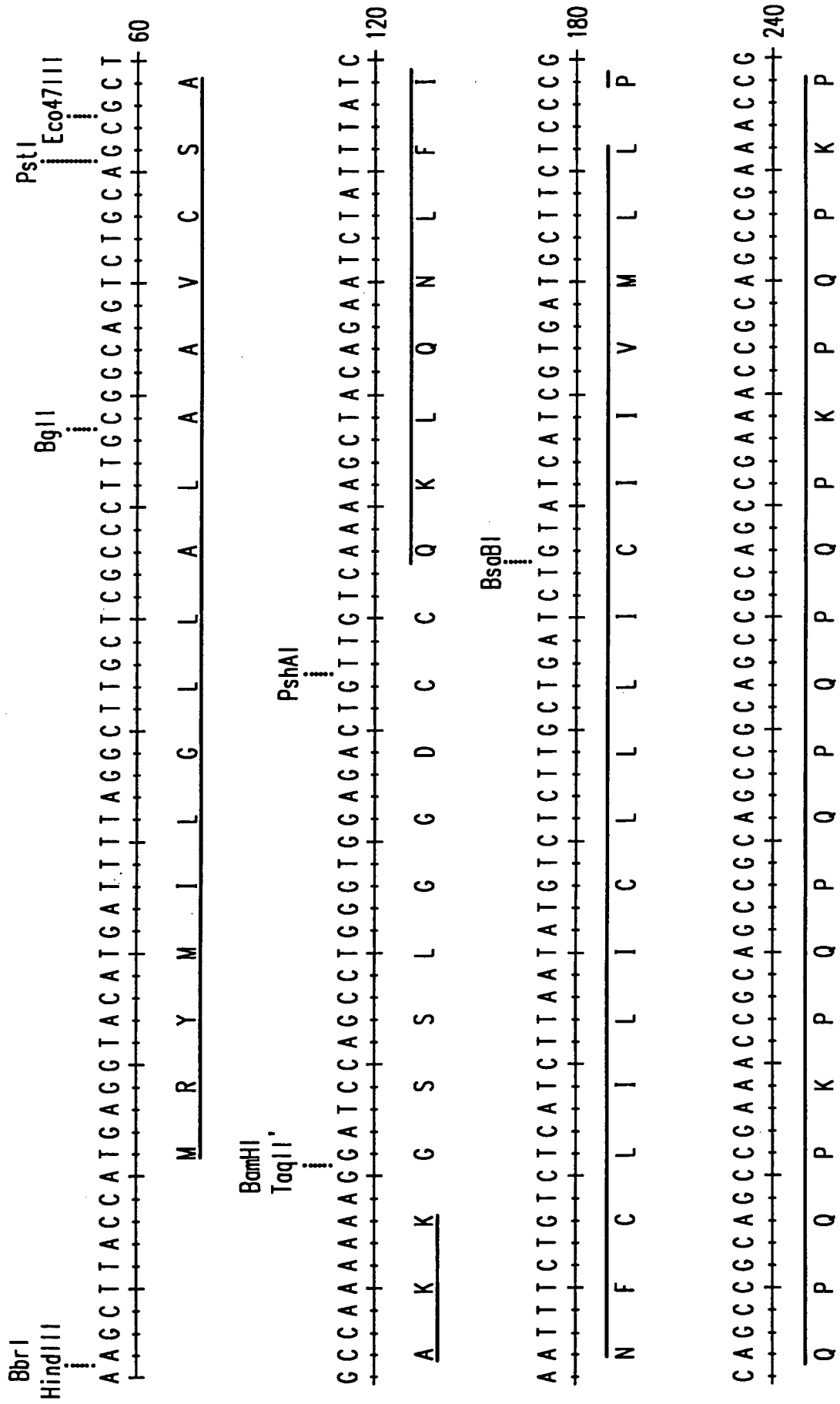


FIG. 7C

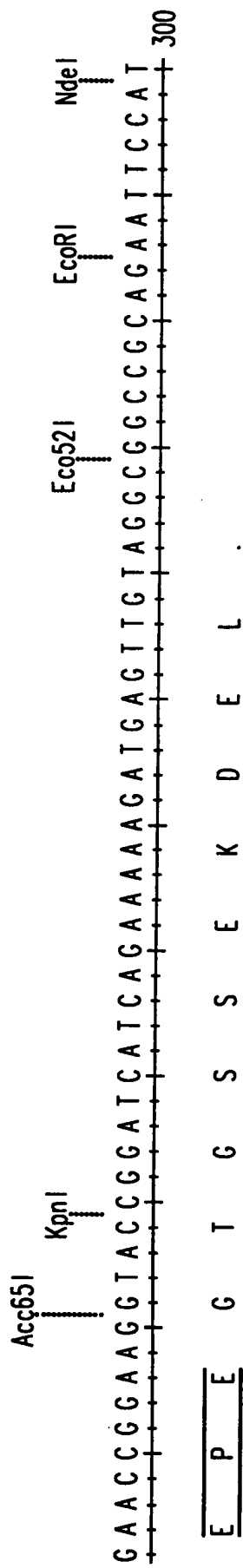
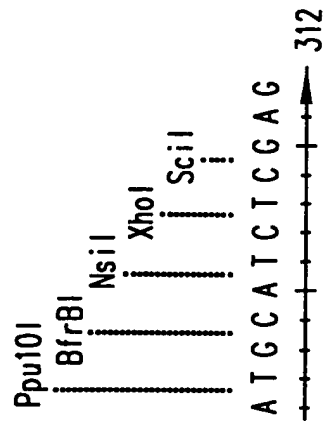


FIG. 7D



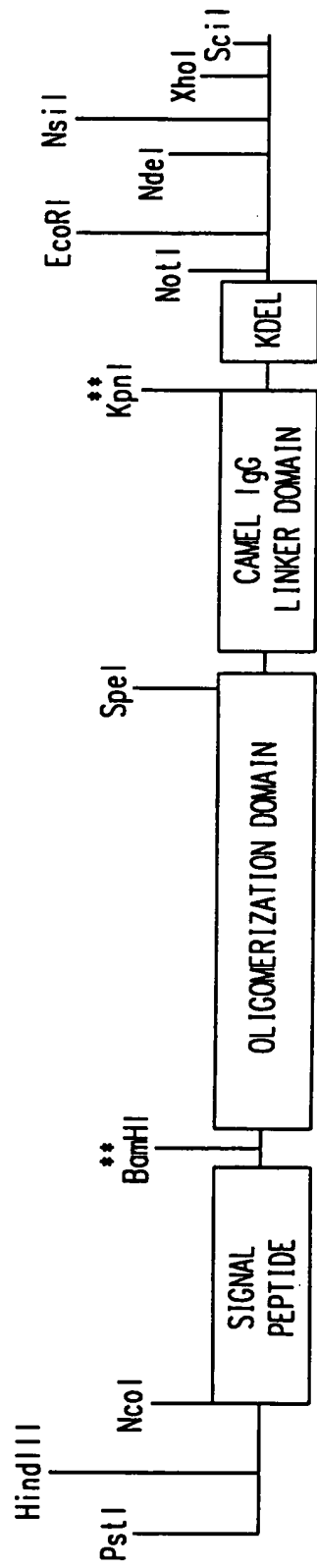


FIG. 8A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - G E Q T K A L V I Q L T L F N Q I L V E L R D D I R D Q V K E M S L I R N T I M E C Q V C G -

P Q P Q K P Q P Q P Q P K P Q K P E P E - G T G S S E - K D E L

FIG. 8B

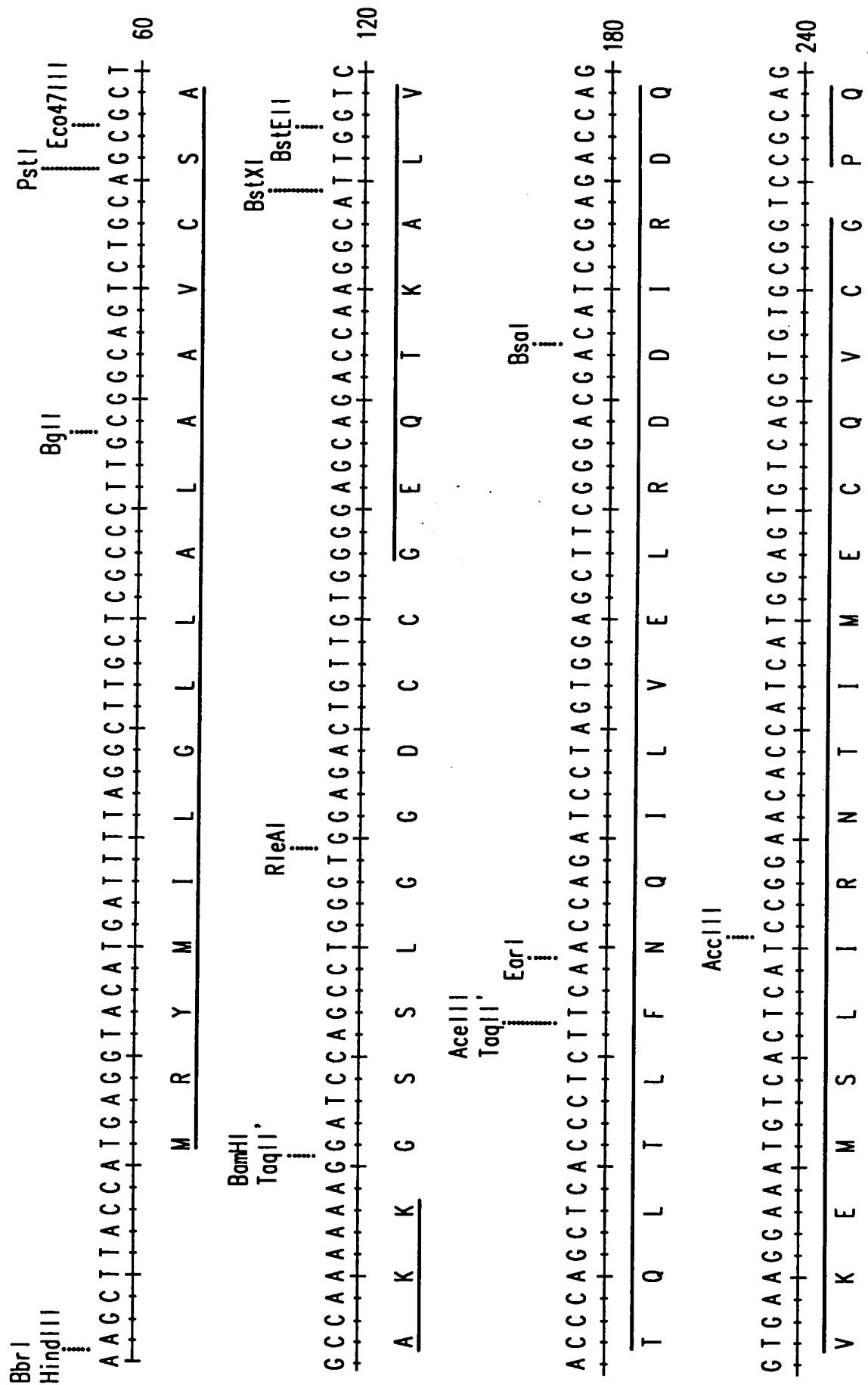


FIG. 8C

CCGAGCCGAAACCGCAGCCCGCAGCCCGCAGCCCGA

CCGAGCCGAAACCGCAGCCCGCAGCCCGCAGCCCGAACCGCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P Q P Q P Q P E

+

CCGGAAGGTACCGGATCATCAGAAAAGATGAGTTGTAGCGCGCGCAGCAATTCCATATG 360

Acc65I KpnI Eco52I EcoRI NdeI Ppu10I BfrBI

P E G T G S S E K D E L

NsiI XhoI SclI CATCTCGAG 369

FIG. 8D

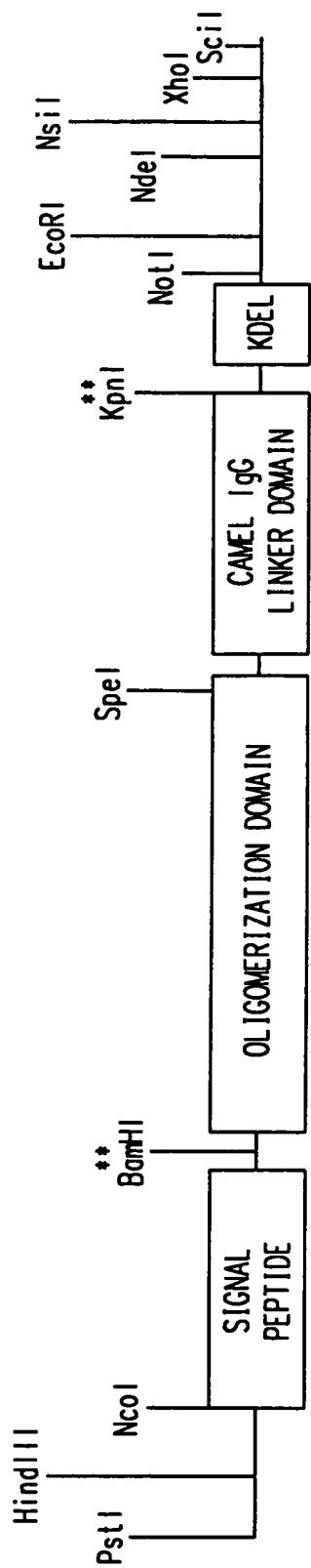


FIG. 9A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - G D F N R Q F L G Q M T Q L N Q L L G E V K D L L R Q Q V K E T S F L R N T I A E C Q A C G -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 9B

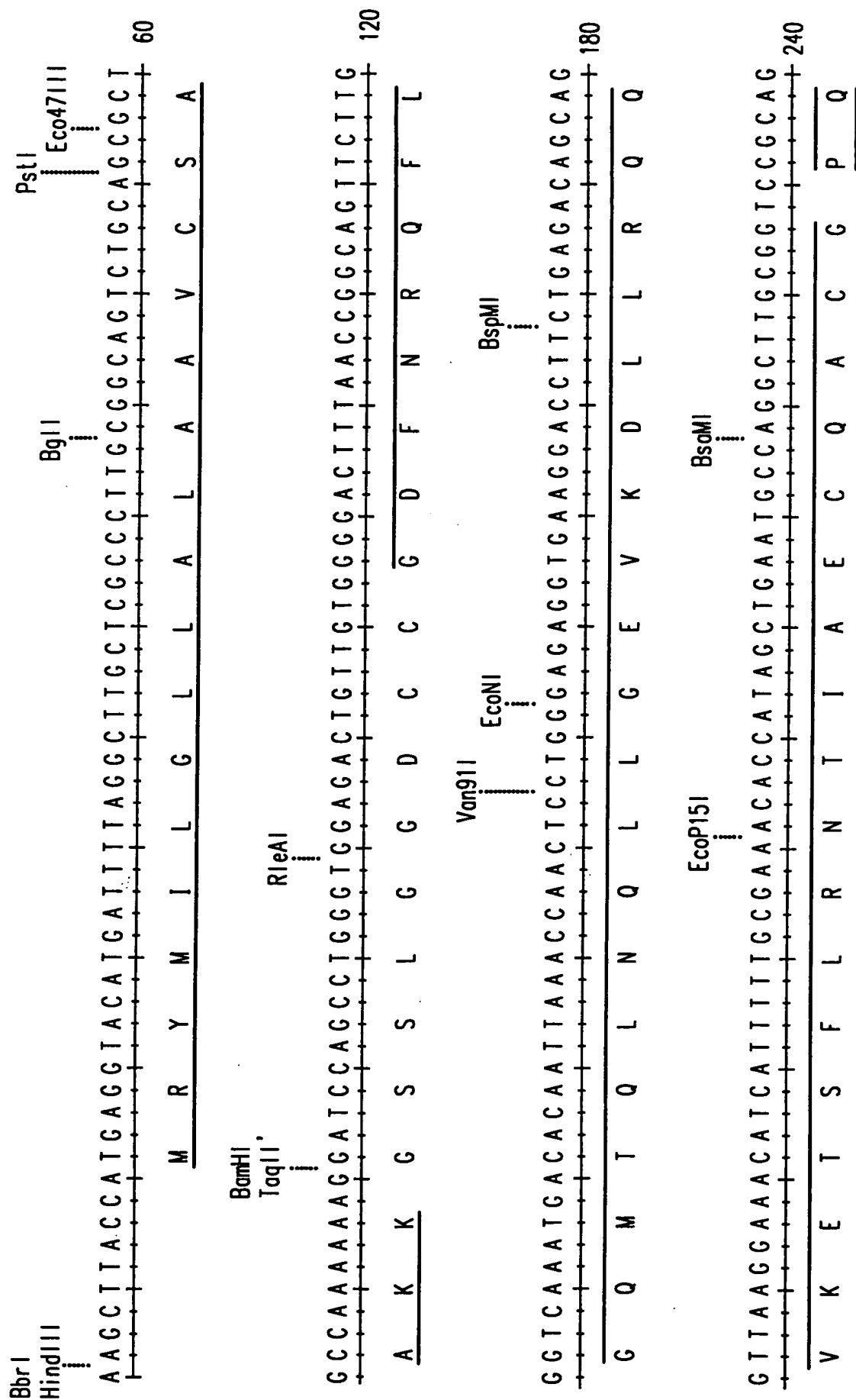


FIG. 9C

CCGAGCCGAAACCGCAGCCGCGCAGCCGCGAACCAGCCGAAACCGGAA 300

P Q P K P Q P Q P Q P Q P Q P Q P K P E

CCGAGCCGAAACCGCAGCCGCGCAGCCGCGAACCAGCCGAAACCGGAA 300

CCGGAAGGTACCGGATCATCAGAAAAGATGAGTGTAGCGCGCGCAGAAATTCATATG 360

P E G T G S S E K D E L

NsiI
XhoI
SciI
CATCTCGAG 369

FIG.9D

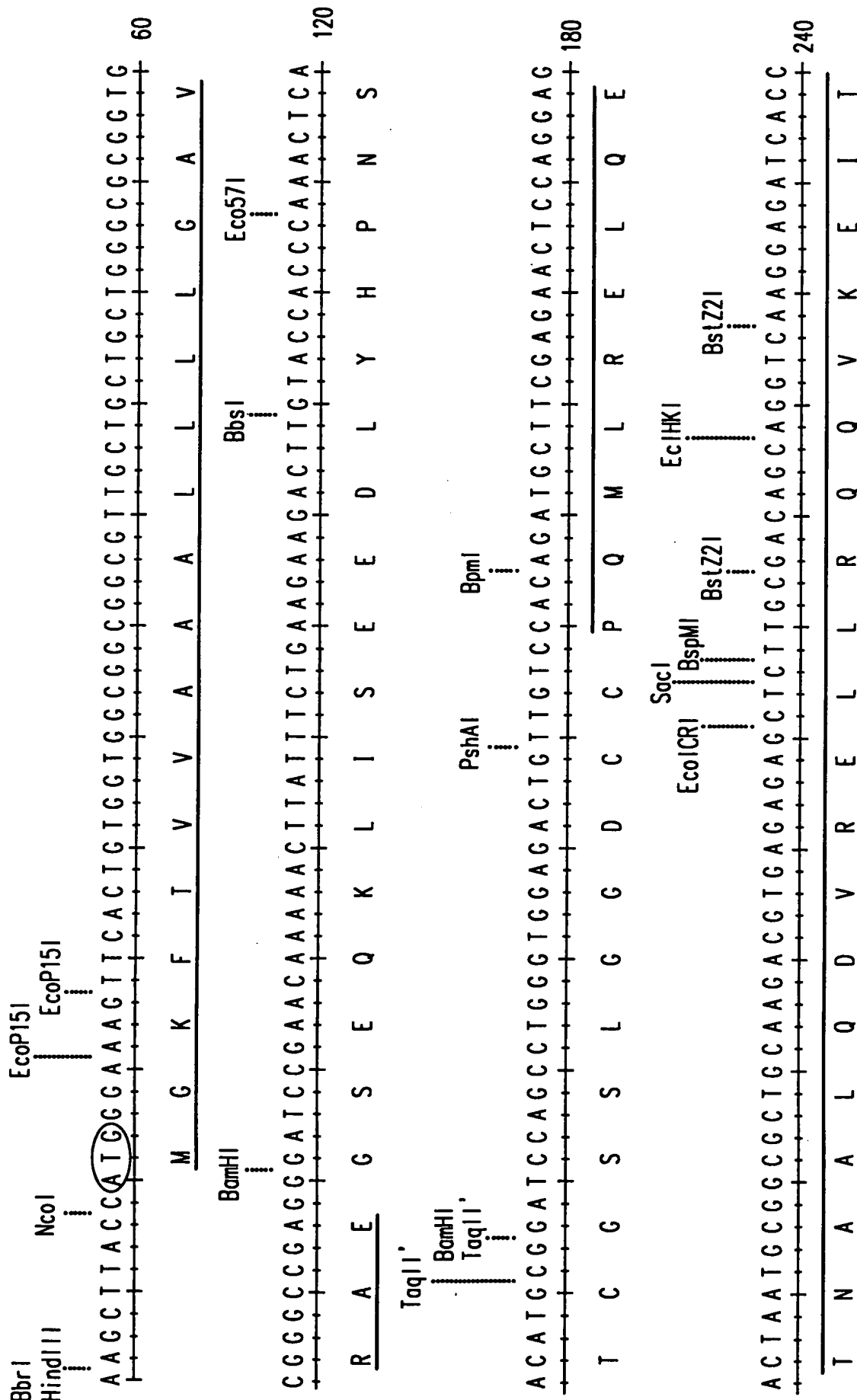


FIG.10C

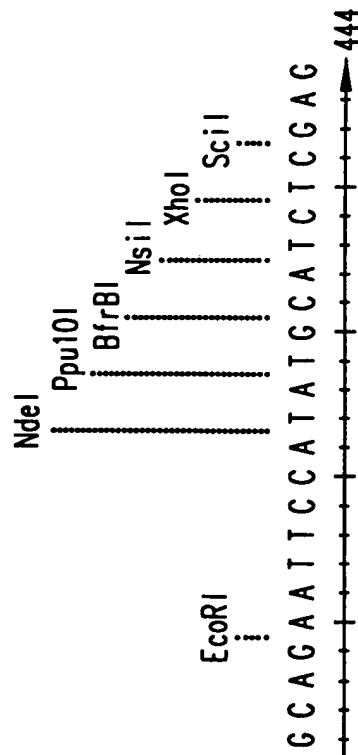
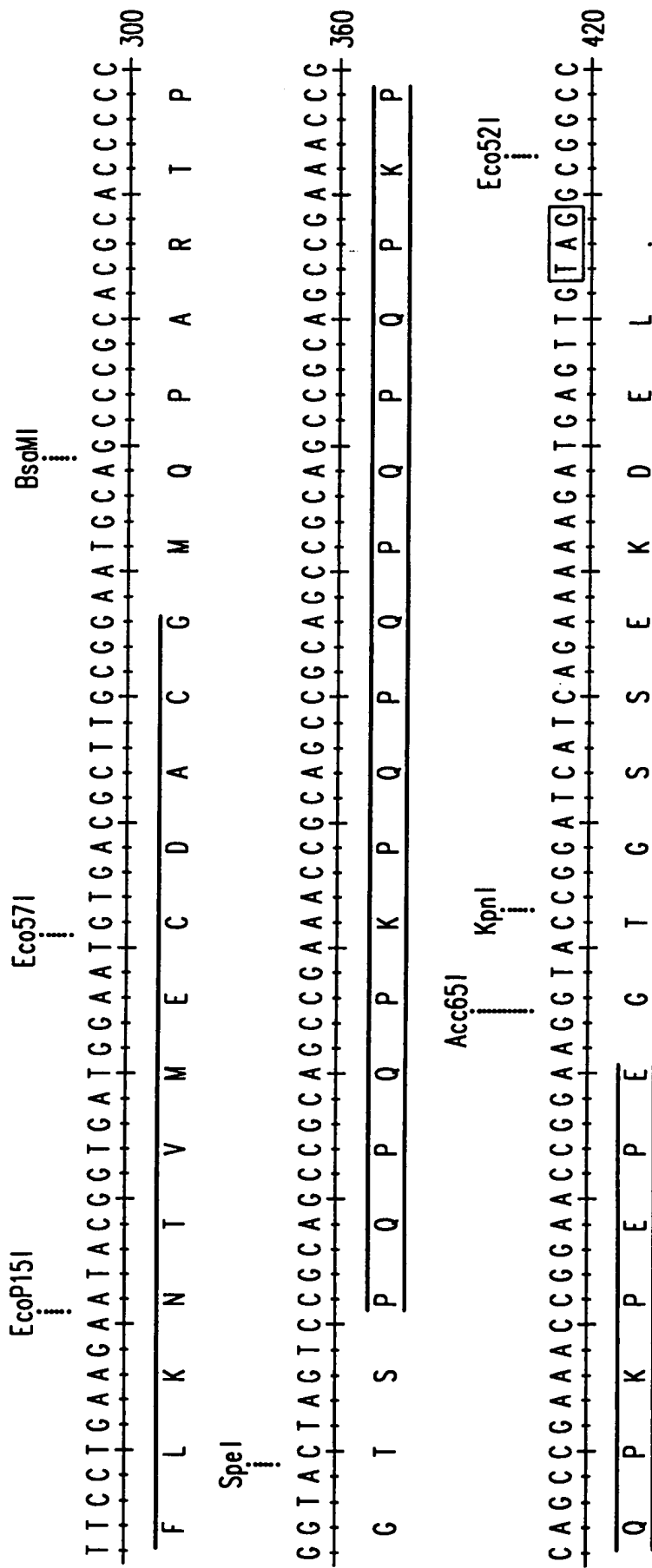


FIG. 10D